

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 03:32:20 ; Search time 310.462 Seconds
(without alignments)
9578.440 Million cell updates/sec

Title: US-10-005-429-13

Perfect score: 700
Sequence: 1 ggaacacacacgggaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
- 6: Geneseq2002as.*
- 7: Geneseq2003as.*
- 8: Geneseq2003bs.*
- 9: Geneseq2003cs.*
- 10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	26.9	540	ADC06863	Adc06863 Plasmid p
2	195.6	26.5	585	AAQ78205	Aaq78205 Gene codi
3	185.6	26.5	687	AAQ6375	Aaq6375 Rice thio
4	184.8	26.4	660	ADC08864	Adc08864 Plasmid p
5	172.8	24.7	659	ADC08860	Adc08860 Plasmid p
6	137.2	19.6	318	ABX87408	Abx87408 Corn ear-
7	120	17.1	382	AAQ62456	Aaq62456 Wheat thi
8	119.6	17.1	393	AAQ10451	Aaq10451 Hard whea
9	119.6	17.1	393	AAQ62457	Aaq62457 Wheat thi
10	119.4	17.1	287	ABL75545	Ab175545 Corn tass
11	119.2	17.0	384	AAQ10450	Aaq10450 Soft whea
12	118	16.9	369	AAQ61537	Aaq61537 Nucleotid
13	118	16.9	369	AAQ59629	Aad59629 Barley th
14	113.6	16.2	278	ABX87380	Abx87380 Corn ear-
15	108.6	15.5	370	AAQ62455	Aaq62455 Barley th
16	103.2	14.7	297	ADC06862	Adc06862 B2 PCR fr
17	100.8	14.4	366	ADA70643	Ada70643 Rice gene
18	100.6	14.4	489	AAQ48089	Aaq48089 Zea mays
19	100	14.3	480	AAQ35542	Aaq35542 Arabidops
20	100	14.3	524	AAQ33829	Aaq33829 Arabidops
21	100	14.3	563	AAQ34211	Aaq34211 Arabidops
22	98.8	14.1	574	AAZ51738	Aaz51738 Catalpa s
23	98.4	14.1	357	ABZ13931	Abz13931 Arabidops

24	98.4	14.1	357	7	ADA67904	Arabidops
25	98.4	14.1	652	3	AAQ48656	Arabidops
26	97.8	14.0	614	3	AAZ51741	Vernonia
27	97.4	13.9	509	5	AAH87768	Peppermin
28	97.4	13.9	572	3	AAQ52069	Arabidops
29	96.2	13.7	601	3	AAZ51740	Glycine m
30	94.6	13.5	590	3	AAQ38792	Arabidops
31	93.6	13.4	576	7	ABX56868	Arabidops
32	93	13.3	360	6	ABZ12359	Arabidops
33	93	13.3	560	3	AAQ41961	Arabidops
34	91.8	13.1	328	3	AAQ31097	Plant mic
35	91.2	13.0	320	3	AAQ31785	Plant mays
36	91.2	13.0	594	3	AAQ48156	Zea mays
37	90.6	12.9	452	3	AAQ46727	Zea mays
38	89.8	12.8	345	6	ABZ12358	Arabidops
39	89.8	12.8	345	6	ABN89587	Arabidops
40	89.8	12.8	561	3	AAQ51522	Arabidops
41	89.8	12.8	563	3	AAQ34121	Arabidops
42	89.8	12.8	3129	6	ABN89579	Phaseolin
43	89.8	12.8	3129	6	ABN89579	Phaseolin
44	89.8	12.8	3888	6	ABN89581	Phaseolin
45	89.8	12.8	3888	6	ABN89580	Phaseolin

ALIGNMENTS

RESULT 1

ADC06863

ID ADC06863 standard; DNA; 540 BP.

XX

AC ADC06863;

XX

DT 18-DEC-2003 (first entry)

XX

DE Plasmid pDONR201 containing the modified rice thioredoxin H DNA.

XX

XW cloning; recombination method; ds; plasmid pDONR201; rice; thioredoxin H.

XX

OS Synthetic.

OS Unidentified.

OS Oryza sativa.

XX

PN US2003143618-A1.

XX

PD 31-JUL-2003.

XX

PF 23-JAN-2003; 2003US-00349782.

XX

PR 23-JAN-2002; 2002EP-00075373.

XX

PA (HATZ/) HATZFELD Y.

PA (FRAN/) FRANKARD V M.

PA (DROU/) DROUAL A.

PI

Hatzfeld Y, Frankard VM, Droual A;

WPI; 2003-671205/63.

XX

PT Producing a modified, chimeric, or reconstructed DNA molecule of two parts comprises amplifying the two DNAs by PCR using primers incorporating recombination sites, ligating the PCR products, and then cloning the ligated products.

XX

PT Disclosure; Fig 5; 15pp; English.

XX

The invention relates to a novel method for producing a modified, chimeric, or reconstructed DNA molecule composed of 2 parts. The method comprises PCR amplification of each part using two primer sets that build in recombination sites at the outer ends of each PCR product, ligating the two PCR products and cloning the ligated products into a recombination vector. The method of the invention may be useful for the easy cloning and selection of chimeric DNA molecules. Unlike classical

even up low
See identity, still
a thioredoxin h

QY	278	CATGTGATCCGACGCTTCGCTTCATCAGGACGGGAGACGCTCGAGAGCTTGGCTACC	337
Db	367	GAGGCAATCCGACCTTCTATT-ATCAAGGATGGTGTGAGGCTGACAGGTGCTGGC	425
QY	338	GTGACGAGGACGAGCTCCGGACGCGCTCAGGAAATACGCGCCGCTGCGCACTACGACG	397
Db	426	GCCAGGAGGATGACCTCCAGAACCACTCGTGAAGACGCTCGGTGCCACTGCTGCTCATCT	485
QY	398	GCTCCTGCTCGGCTGGCTCCG	417
Db	486	GCTTCTGCTTAAGAAATCTC	505

RESULT 6
 AEX87408
 ID AEX87408 standard; cDNA; 318 BP.
 XX
 AC AEX87408;
 XX
 DT 24-APR-2003 (first entry)
 XX
 DS Corn ear-derived polynucleotide (cpd) #5868.
 XX
 KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
 KW structural gene; functional gene; regulatory gene;
 KW corn ear-specific profile; gene transcription; gene expression;
 KW hybrid plant; desirable trait expression; plant breeding program;
 KW inheritance; desirable characteristic; growth; development;
 KW disease resistance; environmental adaptability; quality; yield;
 KW multigene trait; plant; gene; ss.
 XX
 OS Zea mays.
 XX
 PN US6476212-B1.
 XX
 PD 05-NOV-2002.
 XX
 PF 14-MAY-1999; 99US-00313294.
 XX
 PR 26-MAY-1998; 98US-0086722P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lalgudi RV, Ito LY, Sherman BK;
 XX WPI; 2003-208840/20.
 XX
 PT Novel purified corn-ear derived polynucleotide useful as hybridization
 PT probe for detecting polynucleotide in sample, and for identifying,
 PT evaluating, and altering desired characteristics associated with growth,
 PT development.
 XX
 PS Example; SEQ ID NO 5868; 390pp; English.

The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022 and SATMON023. Some of the cdps uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotide sequences are useful for detecting cdps in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdps are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridization techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdps are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cdps are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to

QY	38	ATAATGGCGGCGAGGAGGTCCTGATGCGGTGCCACACAGGACGAGTTGACGCC	97
Db	127	ACAATGGCGGCGAGGAGGTCCTGATGCGGTGCCACACAGGACGAGTTGACGCC	186
QY	98	CCATGGCCCAAGCCAGGACGAGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC	157
Db	187	CAGATGACCAAGCCAGGACGAGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC	246
QY	158	TGCAGTGGGTGCAGATGATGCGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC	217
Db	247	TGTGGCCCTTGGCTTTCATGCGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC	306
QY	218	GCGGTCTTCTCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC	277
Db	307	GCTGCTTCTTCTCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC	366

Query Match 24.7%; Score 172.8; DB 9; Length 659;
 Best Local Similarity 67.6%; Pred. No. 3.5e-20;
 Matches 257; Conservative 0; Mismatches 122; Indels 1; Gaps 1;
 38 ATAATGGCGGCGAGGAGGTCCTGATGCGGTGCCACACAGGACGAGTTGACGCC 97
 127 ACAATGGCGGCGAGGAGGTCCTGATGCGGTGCCACACAGGACGAGTTGACGCC 186
 98 CCATGGCCCAAGCCAGGACGAGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC 157
 187 CAGATGACCAAGCCAGGACGAGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC 246
 158 TGCAGTGGGTGCAGATGATGCGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC 217
 247 TGTGGCCCTTGGCTTTCATGCGGTCGATGCGGTGCCACACAGGACGAGTTGACGCC 306
 218 GCGGTCTTCTCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 277
 307 GCTGCTTCTTCTCGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 366

Producing a modified, chimeric, or reconstructed DNA molecule of two parts comprises amplifying the two DNAs by PCR using primers incorporating recombination sites, ligating the PCR products, and then cloning the ligated products.

Disclosure; Page 7; 15pp; English.

The invention relates to a novel method for producing a modified, chimeric, or reconstructed DNA molecule composed of 2 parts. The method comprises PCR amplification of each part using two primer sets that build in recombination sites at the outer ends of each PCR product, ligating the two PCR products and cloning the ligated products into a recombination vector. The method of the invention may be useful for the easy cloning and selection of chimeric DNA molecules. Unlike classical recombination methods the new method avoids the need for initial cloning using restriction enzymes and allows the production of mutated and/or chimeric DNA molecules. The current sequence is that of the plasmid pDONR201 of the invention which contains the rice thioredoxin H DNA.

Sequence 659 BP; 172 A; 159 C; 159 G; 169 T; 0 U; 0 Other;

(INRG) INST NAT RECH AGRONOMIQUE.

Gauthier M, Lullien-Pellerin V, De Lamotte F, Joudrier P;
WPI; 1996-117050/12.
P-PSDB; AAR93017.

New thioredoxin h from hard and soft wheat - useful e.g. as flour additive or for inactivating toxins, also related nucleic acid, vectors, transformed cells, etc.

Claim 8; Page 34; 50pp; French.

AAT10451 encodes hard wheat thioredoxin h (Thh). Thioredoxin h from hard or soft wheat or other plant is useful as a food additive to improve flour quality or to suppress the anti-nutritional effects of leguminous plants. A further use is to inactivate toxins, esp. bee or snake venom. cDNA clones encoding Thh (pW1333 encodes soft wheat Thh and pW14132 encodes hard wheat Thh) were selected using a Thh probe which achieves specific and accurate selection. The clones may be used in the recombinant prodn. of Thh which produces a higher yield than extraction from wheat. Thh contg. cells can be used directly in food processing. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 393 BP; 82 A; 105 C; 133 G; 73 T; 0 U; 0 Other;

Query Match 17.1%; Score 119.6; DB 2; Length 393;
Best Local Similarity 59.4%; Pred. No. 2.8e-11;
Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

43 GCGCGCCGAGGAGGTCGCGTGCCTGCGTGCACACCAAGAGGATTCGACGCCCGCAT 102
48 GCGCGTGGCGGCGGAGGATTCGCTCCAGCTGAGCAGTGGACCATGCAGAT 107
103 GCGCCAGGCCAAGGAGGAGGAGGTCGCTGATCGCTGCACACCAAGAGGATTCGACGCCCGCAT 162
108 CGAGGAGGCCAAGCGCGGCGGAGGATTCGCTCCAGCTGAGCAGTGGACCATGCAGAT 167
163 TGGGTGCGCAGATGATGGCCCGCGTGTACCGGATGTCGCCAGCAAGTACCCCTTCGCGGT 222
168 ACCATGCGCATTAATAGGCTCCAAATTTTGTCTGATCTCGCCAAAGATTCGACGTCGTGT 227
223 CTTCCTCGAGGTCGACGTCGACGAGTCTGCTGATCGCTGCACACCAAGAGGATTCGACGCCCGCAT 282
228 TTTCTCAAGGTCGACGTCGACGAGTCTGATGAATGAAGCCCATTCAGCCATTCAGCGTCGAGGC 287
283 GATGCGGACCTTCGCTTCATCAGCAAGAGCGGAGCGCTCAGAGCTTTGTACCGTCGA 342
288 CATGCCAACCTTCCTGTTTCATGAGGAGGAGAGCTCAAGGACAGGGTTGTTCGAGCTAT 347
343 CGAGGACGAGCTCCGGGAGCGCGTCAGGAAGTACCGCCCGC 384
348 CAAGGAGGAGCTGACGACCAAGTTGGGCTCCACCGCGCTGC 389

RESULT 9
AAC62457
ID AAC62457 standard; cDNA; 393 BP.
XX AAC62457;
XX 07-FEB-2001 (first entry)
XX Wheat thioredoxin h coding sequence #2.
XX DE
XX Wheat; thioredoxin h; disulfide bridge reduction; development;
XX KW hair care product; venom neutralisation; food technology; food allergy;
XX KW ss.
XX Triticum aestivum.
XX OS
XX WC000050352.32

Db 216 CAGSTCGTCTTCTCGAAGGTGGACGTGGACGAA 248

RESULT 11
AAT10450
AAT10450 standard; cDNA to mRNA; 384 BP.

XX
AC AAT10450;

XX
AC AAT10450;

DT 25-MAR-2003 (revised)

DT 20-SEP-1996 (first entry)

XX
DE Soft wheat thioredoxin h cDNA.

XX
DE DE

XX
DE DE

KM Thioredoxin h; hard wheat; soft wheat; food additive; flour quality;

KM toxin inactivation; venom; ds.

XX
XX

OS Triticum aestivum.

XX
XX

FF Key Location/Qualifiers

FT CDS 1..384

FT /tag= a

FT /product= "thioredoxin_h"

XX
XX

FN WO9603505-A1.

XX
XX

PD 08-FEB-1996.

XX
XX

PF 26-JUL-1995; 95WO-FR001005.

XX
XX

PR 26-JUL-1994; 94FR-00009235.

XX
XX

PA (INRG) INST NAT RECH AGRONOMIQUE.

XX
XX

PI Gauthier M, Lullien-Pellerin V, De Lamotte F, Joudrier P;

XX
XX

DR WPI; 1996-117050/12.

DR P-PSDB; AAR93016.

XX
XX

PT New thioredoxin h from hard and soft wheat - useful e.g. as flour additive or for inactivating toxins, also related nucleic acid, vectors, transformed cells, etc.

XX
XX

PS Claim 7; Page 25-26; 50pp; French.

XX
XX

CC AAT10450 encodes soft wheat thioredoxin h (Thh). Thioredoxin h from hard or soft wheat or other plant is useful as a food additive to improve flour quality or to suppress the anti-nutritional effects of leguminous plants. A further use is to inactivate toxins, esp. bee or snake venom. cDNA clones encoding Thh (pTAM1338 encodes soft wheat Thh and pTAM14132 encodes hard wheat Thh) were selected using a Thh probe which achieves specific and accurate selection. The clones may be used in the recombinant prodn. of Thh which produces a higher yield than extraction from wheat. Thh contg. cells can be used directly in food processing. (Updated on 25-MAR-2003 to correct PI field.)

XX
XX

SQ Sequence 384 BP; 84 A; 98 C; 129 G; 73 T; 0 U; 0 Other;

Query Match 17.0%; Score 119.2; DB 2; Length 384;
Best Local Similarity 59.4%; Pred. No. 3.3e-11;
Matches 202; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

Qy 43 GGGGGCCGAGGAGGTGCCGTGATCGCGTCCACACCCAGGACAGTTCGACGCCCGCAT 102
|||||

Db 39 GCGGTAGGGCGGGGAGGTGATCTCGTCCACAGCCTGGAGCAGTGGACCATGCAGAT 98
|||||

Qy 103 GGCCAGAGCCAGGAGCAGGGCAGCTGGTGGTATCATGACTTATGCCCCCTGTGCAG 162
|||||

Db 99 CGAGGAGGCCAACGCCGCCCAAGAGCTGGTGGTATGACTTCACTCATCATGTGGTCGG 158
|||||

Qy 163 TGGGTGCACATATGCCCCCGGTGTACGCGGACTCGGCCACGAAAGTACCCCTTCGCGGGT 222
|||||

Db 159 ACCATGCGCATTAAGCTCGATTTTCGTGATCTGCCCAAGAGTTCACAGCTGCTGT 218
|||||

XX	WPI: 2003-662517/52.
DR	P-PSDB; AAE39220.
DR	
XX	
XX	New transgenic plants with elevated thioredoxin levels, useful for
PT	producing plant flour or food products with reduced allergenicity and
PT	increased digestibility, or for improving seed germination that results
PT	in high yields in crops.
PT	
XX	
PS	Example 5; Fig 20; 91pp; English.
XX	
CC	The invention relates to a transgenic plant, where part(s) of the plant
CC	comprising a recombinant nucleic acid having a promoter active in such
CC	part(s) operably linked to a nucleic acid encoding a thioredoxin
CC	polypeptide, where the promoter is a seed or grain maturation-specific
CC	promoter. The transgenic plant is useful for generating plants that over
CC	express thioredoxin, as well as plants with reduced thiol groups on
CC	protein(s) such as alpha-amylase inhibitor, alpha-amylase/trypsin
CC	inhibitor, or sulphur-rich gliadin families of proteins. These proteins,
CC	such as the alpha-amylase inhibitor, are allergens that may cause
CC	allergic diseases (e.g. baker's asthma) in individuals. The transgenic
CC	plant is particularly useful for improving seed germination to establish
CC	strong growth and high yields in crop plants, or producing seeds with
CC	improved germination rates. The transgenic plant is also useful for
CC	producing plant flour and food products with reduced allergenicity and
CC	increased digestibility. The present sequence is barley thioredoxin h DNA
XX	
XX	Sequence 369 BP; 83 A; 95 C; 119 G; 72 T; 0 U; 0 Other;

Query Match	16.9%	Score 118	DB 9	Length 369
Best Local Similarity	59.1%	Pred. No. 5.2e-11		
Matches 202	Conservative 0	Mismatches 140	Indels 0	Gaps 0
QY	43	GGCGCGGAGAGGGTGGCGTGGATCGGTGCCACACAGGACGAGTTTCGACGCCCGCAT	102	
DB	21			
QY	103	GCCCAAGGCCAAGGAGCAGGGCAAGCTGGTGGTTCATCGACTTCATGGCCCCCTGGTGCAG	162	
DB	81			
QY	163	TGGGTGCCAGATGATGATGCCCGCGGTGACGCGGACTGCGCAGCAAGTACCTTTCGGCGGT	222	
DB	141			
QY	223	CTTCCTCGAGGTGCAAGCTGCACAGACTGTCTGGAACTGCGGAGATCTACGGCGTCCATGT	282	
DB	201			
QY	283	GATCGCGACCTTCTGTTCATCAGGAAACGGCGAGACGCTCGAGAGCTTTGCTACCGTCGA	342	
DB	261			
QY	343	CGAGACAGAGCTCCGGACGCCGTCACGAAATGACGCCCGCGC	384	
DB	321			
QY	321	CARGAGGAACTGACGCCCAAGGTGTGGCTTTCACGGCGCGCGC	362	
DB				

RESULT 14	
ABX87380	
ID	ABX87380 standard; cDNA; 278 BP.
XX	
AC	ABX87380;
XX	
DT	24-APR-2003 (first entry)
XX	
XX	Corn ear-derived polynucleotide (cpd) #5840.
DE	
XX	
XX	Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
KW	structural gene; functional gene; regulatory gene;
KW	corn ear-specific profile; gene transcription; gene expression;
KW	hybrid plant; desirable trait expression; plant breeding program;
KW	inheritance; desired characteristic; growth; development;
KW	

KW	disease resistance; environmental adaptability; quality; yield;
XX	multigene trait; plant; gene; ss.
KW	Zea mays.
XX	
XX	US6476212-B1.
XX	
XX	05-NOV-2002.
XX	
XX	14-MAY-1999; 99US-00313294.
PF	
XX	26-MAY-1998; 98US-0086722P.
XX	
XX	{INCY-} INCYTE GENOMICS INC.
XX	
XX	Lalquadi RV, Ito LY, Sherman BK;
PI	
XX	WPI; 2003-20884D/20.
XX	
XX	Novel purified corn-ear derived polynucleotide useful as hybridization
PT	probe for detecting polynucleotide in sample, and for identifying,
PT	evaluating, and altering desired characteristics associated with growth,
PT	development.
XX	
XX	Example; SEQ ID NO 5840; 390bp; English.
PS	

The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (zea mays) cDNA libraries SATMONQ22 and SATMONQ23. Some of the cpds uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cpds are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridization techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cpds are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cpds are also useful as molecular markers for studying inheritance and multigenic traits in a plant breeding program. The cpds are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived polynucleotides (cpds) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/?psipdsIDEntry.html

Query Match	16.2%;	Score 113.6;	DB 7;	Length 278;
Best Local Similarity	71.6%;	Pred. No. 2.8e-10;		
Matches 149;	Conservative	0;	Mismatches -59;	Indels 0; Gaps 0;
36	GAATAATGCGCGCGAGGAGGGTGCCTGATCGCGTGCACACCAAGGACGAGTTTCGACG	95		
41	GATCAATGGGTTCCGAGCAGGAGATCGTGATCGGTGCCAGCAAGCGTGAAGTTTCGACG	100		
96	CCCGCATGCGCAAGGCGCAAGGAGCAGGCGCAAGCTGGTGGTTCATCGACTTCATGGCCCCCT	155		
101	CCCACATGACCAAGGCCCAAGGAAGCGGCAAGCTGGTGGTTCATCGACTTCATCGCGCCT	160		
156	GGTGCAGTGGGTGCCAGATGATGGCCCCGGTGTACGCGGACTGGCGCCAGCAAGTACGCTT	215		
161	GGTGGCGTTCATGCCCGCGCATCGCCCCACTGTTGTTTCGAACACGCCCAAGAAATTCATT	220		
216	CCGCGGTCTTCCTCGAGGTCCGACGTCGA	243		
221	AGGTGGTCTTCCTGAAGGTGAACGTGGA	248		

Query Match
Best Local S
Matches 149

36	GAATAATGCGGCGCAGGAGGGTGCCTGATCGCGTGCCACCAAGGACGAGTTCGACG	95
41	GATCAATGGCGTCCGAGCAGGAGTCTGTATCGCGTGCCACAGCAAGGCTGAGTTCGACG	100
96	CCCGCATGGCCAAAGCCACGAGGACGGGAGCTGGTTCATCGACTTCAATGCGCCGCCCT	155
101	CCACATGACCAAGGCCACGAGGACGGCAAGCTGGTGTGTCATCGACTTCACTCGCGCCT	160
156	GGTGCAGTGGGTGCCAGATGATGGCCCCGGTGTAGCCGGACTGGCGCAGCAAGTACCGTT	215
161	GGTGGCGTCCATGCCCGGCCATCGGCCCACTGTTGTTCCGAACAGCCCAAGAAATTCATTC	220
216	CCCGCGTCTTCCTCGAGGTTCGACGTGCA	243
221	AGGTGCTCTTCTTGAAGGTGGAACGTGGA	248

QY 282 TGATGCCGACCTTCTGCTTCATCAGGACGGCGAGACGCTCGAGAGCTTTGCTACCGTCG 341
DB 261 CCATGCCCAACGTTCTCTGTTTCATGAGGAGGAGAGCGTCAAGGACAGGGTTGTCGGAGCTA 320
QY 342 ACGAGGACGAGCTCCGGGACGCGCTCAGGAACTACGCCGCCGC 384
DB 321 TCNAGGAGGAGTACCGGCCAAGGTTGGCTTCACGCGCGGCGC 363

Search completed: May 5, 2004, 21:08:21
Job time : 314.462 secs

RESULT 15
AAC62455
ID AAC62455 standard; cDNA; 370 BP.
XX
AC AAC62455;
XX
DT 07-FEB-2001 (first entry)
XX
XX Barley thioedoxin h coding sequence.
DE
XX Barley; thioedoxin h; disulfide bridge reduction, development;
KW hair care product; venom neutralisation, food technology; food allergy;
KW ss.
XX
OS Hordeum vulgare.
XX
XX WO2000058352-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US008566.
XX
XX 31-MAR-1999; 99US-0127198P.
PR 06-DEC-1999; 99US-0169162P.
PR 21-JAN-2000; 2000US-017739P.
PR 21-JAN-2000; 2000US-017740P.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Cho M, Del Val G, Caillau M, Lemaux PG, Buchanan BS;
XX
XX WPI; 2000-679291/66.
DR P-PSDB; AAB23247.
XX
XX Recombinant or isolated nucleic acid, useful for producing transgenic
PT plants with altered redox properties, encode thioedoxin h or thioedoxin
PT reductase.
XX
XX Claim 60; Fig 2; 125pp; English.
PS
XX The present invention relates to the isolation and use of the barley
CC thioedoxin h coding and protein sequences, the former of which is shown
CC here. These were isolated using the corresponding sequences from wheat.
CC Thioedoxin is thought to be involved in plant development via its
CC function in the reduction of disulfide bridges. Thioedoxin can be used
CC in hair care products and in the neutralisation of some venoms and
CC toxins, and is also useful in the reduction of some food, for example it
CC can be used to reduce the allergenicity of foods and the digestibility of
CC some proteins. It can also be used to enhance the baking qualities of
CC cereal flour
XX
SQ Sequence 370 BP; 83 A; 95 C; 119 G; 73 T; 0 U; 0 Other;
Query Match 15.5%; Score 108.6; DB 3; Length 370;
Best Local Similarity 59.2%; Pred. No. 1.9e-09;
Matches 203; Conservative 0; Mismatches 139; Indels 1; Gaps 1;
QY 43 GCGGCCCGAGGAGGTGCGGTGATCGC-GTCCACACCAAGCAGAGTTGCAACCCGCA 101
DB 21 GCGGCCAGTGGCGGCGAGGTGATCTCGTTCACAGCCTGGAGCAGTGGACCATGCAGA 80
QY 102 TGGCCACGCCAAGCAGGAGGAGCTGCTGATCGTTCATGCTGCTGCTGCTGCTGCTGCA 161
DB 81 TCGAGGAGGCCAACACACCCCAAGAGCTGGTGGTGAATGACTTCACTCATCATGCTGCTG 140
QY 162 GTGGGTGTCAGATGATGCCCCGCTGTACCGGGAGCTGGCCAGCAAGTACCCCTTCGCGG 221
DB 141 GACCATGCGCATCATGCTCCAGTTTTCGCTGATCTCGCCCAAGAAATTCACCAATGCTG 200
QY 222 TCTTCTCGAGTGCAGCTGTCGAGCACTGCTGGAAGTCCGGAAGATCTACCGCTCCATG 281
DB 201 TTTTCTCAAGGTGAGCTGGATGAATCAAGCCCAATTCCTGAGCAATTCAGTGTGAGG 260

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	195.2	27.9	466	6	AR414207	AR414207 Sequence
2	195.2	27.9	466	6	BD109760	BD109760 EST and e
3	187	26.7	601	8	OSU92541	U92541 Oryza sativ
4	185.6	26.5	600	8	AK059196	AK059196 Oryza sat
5	185.6	26.5	686	6	E08194	E08194 RPS13 gene
6	185.6	26.5	686	6	R1C1H	D21836 Oryza sativ
7	185.6	26.5	733	8	AK121423	AK121423 Oryza sat
8	184	26.3	526	11	G73679	G73679 R248R etio
9	165.6	23.7	598	8	AY072771	AY072771 Trifolium
10	162.4	23.2	357	8	AY245454	AY245454 Hordeum v
11	137.2	19.6	318	6	AR250509	AR250509 Sequence
12	123.4	17.6	664	8	AF323593	AF323593 Prunus pe
13	121.2	17.3	596	8	TAE9762	AJ009762 Trifolium
14	120.6	17.2	371	11	G71188	G71188 VB028311FM
15	119.6	17.1	393	6	A48516	A48516 Sequence 4
16	119.6	17.1	437	8	AF420472	AF420472 Trifolium
17	119.6	17.1	630	6	A48520	A48520 Sequence 8
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21	119.2	17.0	629	8	TAE404845	AJ404845 Trifolium
22	119.2	17.0	659	6	A48519	A48519 Sequence 7
23	119.2	17.0	670	8	TATHIORDH	X69115 T.aestivum
24	118	16.9	320	8	RICSS396	D21310 Oryza sativ
25	118	16.9	369	8	AY245455	AY245455 Hordeum v
26	115	16.4	1285	8	CRTRXH	X78822 C.reinhardt
27	114	16.3	676	8	AY344230	AY344230 Ipomoea b
28	113.6	16.2	278	6	AR250481	AR250481 Sequence
29	105	15.0	720	8	BT009180	BT009180 Trifolium
30	102.4	14.6	580	8	BNUS9380	US9380 Brassica na
31	102.2	14.6	463	8	AF273844	AF273844 Brassica
32	102.2	14.6	535	8	AB010434	AB010434 Brassica
33	102.2	14.6	544	8	BOPC17	X89759 B.oleracea
34	102.2	14.6	554	8	BNUS9379	US9379 Brassica na
35	101.8	14.5	740	6	AB053294	AB053294 Oryza sat
36	100.8	14.4	366	6	AK654096	AK654096 Sequence
37	100.8	14.4	682	8	AK059385	AK059385 Oryza sat
38	100.8	14.4	3740	8	AK106758	AK106758 Oryza sat
39	100.6	14.4	130372	2	CNS08C9Z	AL772421 Oryza sat
40	100	14.3	639	8	AY085117	AY085117 Arabidops
41	99.8	14.3	784	8	AY271308	AY271308 Citrus x
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43	98.4	14.1	357	6	AX412277	AX412277 Sequence
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45	98.4	14.1	357	6	AX412279	AX412279 Sequence

ALIGNMENTS

RESULT 1
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LOCUS AR414207 466 bp DNA
DEFINITION Sequence 1844 from patent US 6639063.
ACCESSION AR414207
VERSION AR414207.1 GI:40169317
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 466)
AUTHORS Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 1844 28-OCT-2003;
FEATURES Location/Qualifiers

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 13:19:01 ; Search time 2847.79 Seconds
(without alignments)
10653.920 Million cell updates/sec

Title: US-10-005-429-13
Perfect score: 700
Sequence: 1 ggatccacacgaggaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTIFY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb.htg.*
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6: gb.pat.*
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9: gb.pr.*
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11: gb.sts.*
12: gb.sy.*
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15: em.ba.*
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Pred. No. is the number of results predicted by chance to have a

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Qy	96	CCGCGATGCGCAAGGCCAAGGACAGGCGAAGCTGCTGTCTATCGACTTCATCGCCGCCCT	155						
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Qy	216	CGCGGTCTTCTTCGAGTCTGAGCTCGAGCACTGCTGGAAGTCGCGAAGATCTACGGCG	275						
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Db	365	GTGCCAGGAAGCAGCAGCTCTCGGCCAGATCGAGAAGCATGCGCGCGCTTCGCGCTTCGCT	424						
Qy	396	CGGCTCTTCCT 407							
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RESULT 3
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LOCUS      601 bp      mRNA      linear      PLN 09-APR-1997
DEFINITION Oryza sativa thioredoxin h mRNA, complete cds.
ACCESSION U92541
VERSION   U92541.1  GI:1930071
KEYWORDS
SOURCE
ORGANISM  Oryza sativa (indica cultivar-group)
           Oryza sativa (indica cultivar-group)
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 601)
           Lee,N.C., Eun,M.Y. and Lee,G.R.
           Isolation and characterization of thioredoxin h gene from rice
           Unpublished
REFERENCE 2 (bases 1 to 601)
           Lee,M.C. and Eun,M.Y.
           Direct Submission
           Submitted (09-MAR-1997) Cyto genetics, National Institute of
           Agricultural Science and Technology, Se-Dun Dong, Suwon 440-707,
           Korea
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```

12869764
2 (bases 1 to 600)
REFERENCE
AUTHORS
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukaya,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Kawagashira,N., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Inamura,K., Iwano,T., Imotani,K., Ishibiki,J., Ishii,I., Ishikawa,M., Itoh,M., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,K., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narioka,K., Niikura,J., Nishi,K., Nomura,K., Numasaki,P., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Otsuno,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
TITLE
JOURNAL
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp)
Tel:81-29-838-7007, Fax:81-29-838-7007
This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narioka,K., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Inamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Otsuno,N., Oka,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
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Best Local Similarity 66.5%; Pred. No. 3.5e-204;
Matches 266; Conservative 130; Indels 0; Gaps 0;
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71 AGGAATTAGCAGCAGAGAGAGCAATGCGCCGAGAGCGAGTGGTATGCTGCTGCGACA 130

	<p>Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, R., Nagata, T., Nakahama, Y., Nakamura, M., Namiki, T., Nariawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ono, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, S., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shingawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.</p>
TITLE	Collection, mapping, and annotation of 28K full-length cDNA clones from japonica rice
REFERENCE	Unpublished
AUTHORS	3 (bases 1 to 733)
TITLE	Direct Submission
JOURNAL	Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan [E-mail: sk.kuchien@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007]
COMMENT	This clone is one of the 32K full-length cDNA clones from japonica rice.

```

URL : http://cdna01.dna.attic.go.jp/CDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Fotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y
PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M.,
Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M.,
Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M.,
Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M.,
Xie, Q., Yokemizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, I., Arakawa, T., Carnindi, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirohane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K.,
Sakazume, N., Sano, H., Sasaki, T., Sogabe, Y., Tagami, M.,
Shinagawa, A., Shiraki, T., Tagawa, A., Takahashi, F.,
Tagami-Takeda, Y., Tagawa, S., Tanaka, T., Toyaru, A., Waki, K.,
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Yasunishi, A. and Hayashizaki, Y.
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Best Local Similarity 66.5%; Pred. No. 3.6e-20;
Matches 266; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
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Db	334	AGGCTGACAGGTCGTTGGCGCCAGGAAGATGACCTCCAGAACACCATCTGTGAAGCACG	393	
Qy	378	CGCGCGTCGGCACTACGACGGCTCCTGCCTCGCGGTCCGC	417	
Db	394	TCGGTGCACCTCGTCGCACTCTGCTTCGCTTAAGAAATTC	433	

RESULT 7
AK121423
LOCUS
DEFINITION
AK121423
VERSION
KEYWORDS
SOURCE
ORGNISM
Oryza sativa (japonica cultivar-group) cDNA clone:J023133N23, full insert sequence.
AK121423
GI:37991046
FLI CDNA: CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1
REFERENCES
AUTHORS
The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, S., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, S., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, U., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carrinci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayashi, N., Imotani, K., Ishii, Y., Itoh, W., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

2
REFERENCES
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Endo, T., Fukuda, S., Hara, A., Hashizume, W., Hayashi, N., Imotani, K., Ishii, Y., Itoh, W., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
22752273
12869764

JOURNAL	Collection mapping, and annotation of over 28,000 cDNA clones from
MEDLINE	Japanese cDNAs
PUBMED	Sydney 361 (5631), 376-379 (2003)
REFERENCE	22552273
AUTHORS	ADACHI, J., AIZAWA, K., AKIMURA, T., ARAKAWA, T., CARNINCI, P., DOI, K., FUKUMI, T., FUTADA, S., HANAOKI, T., HARA, A., HASHIZUME, W.,

72	AGGAATTAGGAGGAGAGAGAGCAATGGCCCGGAGGAGGTCGTGATCGCGCTGCCACA	131	
QY	CCAAAGGACGAGTTTCGAGCCCGCATGTCGCCAAGGCCAAGCAGCAGGCGCAAGCTGCTGGTCA	137	
Db	132	ACAAAGGACGATTCGACGCCCAAGAGACCAAGGCCAAGCGCGCAAGTGTGTCAATA	191
QY	138	TGCACTTCATGCGCCCCCTGGTCAGTCGGTGCCAGATGATGCGCCCGGTGTACGCGGACT	197
Db	152	TTGACTTCACATGCTTCCTGGTGTGGCCCTTCGCGCTTCATCGCGCCAGATGTTGCGCTGAAT	251
QY	198	CGCGCAGCAAGTACCCCTTCGCGGCTCTTCTCTCGAGGTCGACGCTCGACGAACCTGCTCGGAAG	257
Db	252	ACGCCAAAAGTTCCCTGGGTGCTGTCTCTCTGAAAGTTGATTTGATGAGCTGAAAGGAAG	311
QY	258	TCGGAGAGATTACGGGCTCCATGTATGATGCGGACCTTTCTGCTTCATCAGAACGGCGAGA	317
Db	312	TTGTCTGAAAAGTACAATGTTCGAGGCAATGCCACCTTCCTATTATCATCAAGGATGTCGTG	371
QY	318	CGCTCGAGAGCTTTTGTACCGTCGACGAGCAGCAGCTTCGGGACGCGGTCAGGAAGTACG	377
Db	372	AGGCTGACAGGTCGTTGGCGCCCAAGGAAGATGACCTCCAGACACCAATCGTGTGAGGACCG	431
QY	378	CGCGCGCTGGCACTACGACGGCTCCTGCCTCGCGGTCGCGC	417
Db	432	TCGGTGCACATGCTGCTACTCTGCTTCTCGCTTAAGAAATTC	471

RESULT 8						
G73679						
LOCUS						
ZNF488						
DEFINITION						
RZ488R etiolated leaf tissue of rice Oryza sativa STS genomic clone						
RZ488 sequencing direction=reverse.						
RZ488 sequence tagged site.						
G73679						
526 bp	DNA	linear				
STS 16-JUL-2002						

G73679.1 GI:19697274
 STS.
 ORYZA SATIVA (indica cultivar-group)
 ORYZA SATIVA (indica cultivar-group)
 EUKARYOTA; VARIIDPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 SPERMATOPHYTA; MAGNOLIOPHYTA; LILLOPSIDA; POALES; POACEAE;
 ECHARTOIDEAE; ORYZEAE; ORYZA.

REFERENCE	1 (bases 1 to 526)
AUTHORS	McCouch, S.R.
TITLE	Oryza sativa STS
JOURNAL	Unpublished (2002)

Contact: Susan R. McCouch
Cornell University
Dept. of Plant Breeding, Ithaca, NY 14853-1901, USA
Tel: 6072550420
Fax: 6072556683
Email: srm4@cornell.edu
Primer A: M13 Universal Forward GTAAACGACGGCCAGT
Primer B: M13 Universal Reverse AACAGCTATGACCATG
STS size: 526
protocol:

Template: 20-100ng
 Primer: 5pmol each
 DNTPs: 40nmol
 Tag polymerase: 5units
 Total volume: 50ul
 Buffer:
 Tris-HCl: 100mM
 KCl: 500mM
 MgCl₂: 15mM
 Gelatin: 0.1%
 PH: 8.3

This is a partial sequence of the RfLP clone named above that was mapped at Cornell University Plant Breeding Dept. and sequenced at the Genome Sequencing Center at Cold Spring Harbor Laboratory. This marker is located on rice chromosome 7. For citations and other

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related information concerning this probe, please refer to the
Gramene database at http.
FEATURES
    Location/Qualifiers
        1..526
            /organism="Oryza sativa (indica cultivar-group)"
            /mol_type="Genomic DNA"
            /cultivar="IR36"
            /db_xref="taxon:39946"
            /map="n7"
            /clone="RZ488"
            /clone_lib="etiolated leaf tissue of rice"
            /note="Vector: Lambda ZAP II/pBluescript; V-type: Plasmid;
A Lambda ZAP II DNA library was constructed from mRNA
extracted from etiolated leaf tissue of the rice cultivar
'IR36' and converted to pBluescript (amp resistant) as
described in Causse et al. (1994) Genetics 138:1251-1274.
For insert amplification, Use M13 forward and reverse
primers. Restriction site is EcoRI. Clones from this
library are designated with the prefix 'RZ1.'
        <1..>526
    STS

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STS
 ORIGIN
 <1..526
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 Best Local Similarity 66.2%; Pred. NO. 6.3e-20;

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60	DB	AGGAATTAGGAGGAGAGAGAGCAATGGCCCGCGAGGAGGGAGTCTGTATCGCTGCCACA	119
78	AY	CCAGGAGCAGATTCCGACGCCCGCATGGCCCAAGGCCAAGCAGCAGGCGCAAGCTTGGTGGTCA	137
120	DB	ACAGGAGCAGATTTCGACGCCCGCCAGATGACCAAGGCCAAGGAGGCCGCAAAAGTGGTCATAA	179
138	AY	TCGACTTCATTGCGCCCCCTGGTGCAGTGGGTGGCCAGATGATGGCCCCCGGTGTACGGCGACT	197
180	DB	TTTGACTTCCTACTGCTCCTGGTGGCCCTTGGCGCTTCATCGCCCCCAGTGTTCGCTGAAT	239
198	AY	GGCGCCAGCAAGTACCTTCCGCGGCTTCTCCTCGAGSTCGACGTGCAGCAACTCTCTGGAG	257
240	DB	ACGCCAAAAAGTTCCTGGTGTGTCCTTCCTGAAAGTTGATGTTGATGAGCTCGAAGGAAG	299
258	AY	TGGCGNAGATCTACGGCGTCCATGTGTGATGCGCAGCTTCTGCTTCATCAGCAACGGCGAGA	317
300	DB	TTTCTGAAAAGTACAAATGTTGAGGCCAATGCCACCTTCCTATTCATCAAGGATGGTGTCTG	359
318	AY	CGTCTGAGAGCTTTGCTACCGTTCGACGAGCAGAGCTCCGGGACCGCGTCAGGAAGTACG	377
360	DB	AGGCTGACAGGTGCTTGGCGCCGAGGAGATGACCTCCAGAACACCATCGTGAACACG	419
378	AY	CCGCGCGTCGGCACTAGCAGGGTCTCTGCTTCGGCGTCCGC	417
420	DB	TGGGTGCCACTGCTGCACTGCTGCTTCTGCGCTAAGAAATTC	459

RESULT 9	AY072771	598 bp	mRNA	linear	PLN 01-JAN-2003
LOCUS	AY072771				
DEFINITION	Triticum aestivum cultivar Soissons thioeredoxin H mRNA, complete cds				
ACCESSION	AY072771				
VERSION	AY072771.1	GI:27461139			
KEYWORDS	.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				

[illegible]

```

AUTHORS      Maeda, K., Finnie, C., Ostergaard, O. and Svensson, B.
TITLE        Direct Submission
JOURNAL      Submitted (27-FEB-2003) Chemistry, Carlsberg Laboratory, Gamle
              Carlsberg Vej 10, Copenhagen DK-2500 Valby, Denmark
FEATURES     Location/Qualifiers
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                /cultivar="barke"
                /sub_species="vulgare"
                /db_xref="taxon:112509"
                /dev_stage="embryo"
              1..357
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                VIADPVREYAKKPGGAIFLKVDVDELKDAEAVNVEAMPTFLFKDGEKVDVSVVGGRK
                IDHTKTKVALMGSAFLK"

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Query Match	23.2%	Score 162.4	DB 8	Length 357;
Best Local Similarity	69.6%	Pred. No. 1.8e-16;		
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Qy	41	ATGCGCGCGGAGGAGGTCGCTGATCGCTGCGCCACACCAAGGACGAGTTCGACGCCCGC	100	
Db	1	ATGCGCGCGGAGGAGGCGCGTTATCGCTGCCACACCAAGCAAGATTCGATACCCAC	60	
Qy	101	ATGGCCAAAGGCCAAGGACGAGCGCAAGCTGGTGGTCATCGACTTCATGGCCCCCTGGTGC	160	
Db	61	ATGGCCAAATGCCAAGGACACCGGCAAGCTGGTGATCATTTGATTTTCACTGCTTCCTGGTGC	120	
Qy	161	ATGGGGTCCAGATGATGGCCCGCGGTGTACCGGAGCTCGCCGACGAAGTACCCCTTCGCGG	220	
Db	121	GGTCCATGCTGTGTCATAGCCCCCACTTTGCTGAGTACGCGCAAGAGTTCCCTGGGGCC	180	
Qy	221	GTCTTCTTCGAGGTGCGAGTCCGACGAACTGCTGGAACTCGGAGATCTACGGCGTCCAT	280	
Db	181	ATCTCTCTGAGGTGATGTTGATGAGCTGAAGGACGTGCGTGTGAAGCATACAATGTTGAG	240	
Qy	281	GTGATGCCGACCTTCCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTTGCTACCGTC	340	
Db	241	GCAATGCCGACCTTCCTGCTTTATCAAGACCGTGAAGAAGGTGACAGTGTTCGCGTGC	300	
Qy	341	GACGAGGACGAGCTCC	356	
Db	301	AGGAGGATGACATCC	316	

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RESULT 11
AR250509
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match
19.6%; Score 137.2; DB 6; Length 318;
linear PAT 20-DEC-2002
318 bp DNA
Sequence 5968 from patent US 6476212.
AR250509
AR250509
AR250509.1 GI:27298383
.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 318)
Lalguadi,R.V., Ito,L.Y. and Sherman,B.K.
Polynucleotides and polypeptides derived from corn ear
Patent: US 6476212-A 5868 05-NOV-2002;
Location/Qualifiers
1..318
/organism="unknown"
/mol_type="genomic DNA"

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Matches 204; Conservative 0; Mismatches 130; Indels 0; Gaps 0

QV 43 GGCGCCGAGGAGGTGCGGTGATCGGTGCCACCAAGGACGAGTTCGACGCCGCAT 102

Db 97 GCGGCGGGGGGGGGAGGTGATCTCGTCCACACCTTGGACAGTGGACCATGAGAT 146
Qy 103 GCGCAAGGCCAAGGAGGAGGCAAGCTGGTGGTGCATCGACTTCATGCGCCCGCTGGTGCAG 162
Db 147 CGAGGAGGCCAAGCCCGCAAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 206
Qy 163 TGGGTGCGAGATGATGCGCCCGGTGTCAGCGGAGTGGCCAGCAAGTACCTTCCCGGT 222
Db 207 ACCATGCGCGATCATGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCG 266
Qy 223 CTCTCTCGAGTGCAGCTGCGACCACTGCTGGAAGTGCAGCAAGTCTAGCGGCTCCATGT 282
Db 267 TTCTCTCAAGTGCAGTGTGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 326
Qy 283 GATCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 342
Db 327 CATGCCAACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 386
Qy 343 CGAGGAGGAGTCTCGGAGCGCGCTGCAAGAGTACGCGCGCGCG 384
Db 387 CAAGGAGGAGTCTGCAAGAGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428

RESULT 14
G71188/c 371 bp DNA linear STS 08-JUN-2001
DEFINITION V80228311FM017 maize leaf DNA Zea mays STS genomic, sequence tagged site.
ACCESSION G71188
VERSION G71188.1 GI:14332873
KEYWORDS STS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 371)
Yang, X.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
3' UTR sequences of maize genes
Unpublished (2001)

REFERENCE
AUTHORS Schnable, P.S.
TITLE Schnable laboratory
JOURNAL Iowa State University
COMMENT G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: GCAAGCTGGTGGTCAATG
Primer B: AAGTATCCATGGTTAAGTATCGCC
PCR Profile:
Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
Thermal cycler: Perkin Elmer TC

Protocol:
Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/ul
Total vol: 20 ul
Buffer:
MgCl2: 2 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.4.

FEATURES
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/clone_lib="maize leaf DNA"
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<1. .>371

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ORIGIN
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Best Local Similarity 67.1%; Pred. No. 9e-10;
Matches 171; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
Qy 153 CTCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTCAGCGGAGTGGCCAGCAAGTACC 212
Db 370 CTCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTCAGCGGAGTGGCCAGCAAGTACC 311
Qy 213 CTCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTCAGCGGAGTGGCCAGCAAGTACC 272
Db 310 CTCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTCAGCGGAGTGGCCAGCAAGTACC 251
Qy 273 CGCTCCATGTGATCGCCAGCTTCTGCTTCATCAGAACCGCGGAGACCTCTCGAGAGCTTTG 332
Db 250 AGTTCGAGGCGATGCGGACCTTCCACTTCGTCAGAACCGCGGAGACCTCTCGAGAGCTTTG 191
Qy 333 CTACCGTCGAGGAGGAGCTCGGAGACCGCGCTCAGGAAGTACGCGCGCTGGGACTA 392
Db 190 TGGGTGCGCAGGAGGAGCTCTGCGCCCTGATCGAGAACGATCGCGCGCTGGGACTA 131
Qy 393 CGAGCGCTCTGCGCT 407
Db 130 CGTCTGCGCTGCGCT 116

RESULT 15
A48516
LOCUS A48516
DEFINITION Sequence 4 from Patent WO9603505.
ACCESSION A48516
VERSION A48516.1 GI:2302293
KEYWORDS Triticum turgidum subsp. durum (durum wheat)
SOURCE Triticum turgidum subsp. durum
ORGANISM Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 (bases 1 to 393)
Gauthier, M., Jullien-Pellerin, V., De, L.F. and Joudrier, P.
HARD AND SOFT WHEAT THIOREDOXINS b, HOMOLOGOUS PROTEINS, DNA FRAGMENTS CODING FOR SAID PROTEINS AND METHODS FOR PREPARING SAME
Patent: WO 9603505-A 4 08-FEB-1996;
AGRONOMIQUE INST NAT RECH (IFR)
Other publication AU 3082795 960222
Other publication FR 2723097 960202.
Location/Qualifiers
1. .393
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FEATURES
source 1. .393
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ORIGIN
Query Match 17.1%; Score 119.6; DB 6; Length 393;
Best Local Similarity 59.4%; Pred. No. 1.3e-09;
Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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QY	103	GGCCAAAGGCCAAGGACAGGGCAGCTGGTGCATCGACTTCATGCCCCCTGGTGCAG	162
Db	108	CGAGGAGGCCAAGCGCCCAAGAGCTGGTGGTGAATTGACTTCACTGCATCATGGTGC	167
QY	163	TGGGTGCCAGATGATGGCCCCCGGTGTACGGGACTCGCCAGCAAGTACCTTCCGCGGT	222
Db	168	ACCATGCCGATCATGGCTCCAAATTTTGTGATCTGSCCAAGAGTTCCACAGTGTGT	227
QY	223	CTTCTCGAGGTCGACGTGACGAACTGCTGGAAGTCCGGAAGATCTACGGTCCATGT	282
Db	228	TTTCTCTCAAGGTCGACGTTGATGAAGCCCAATTGCTGAGCAATTGAGGTGAGGC	287
QY	283	GATGCCGACCTTCTGCTTCATCAGGAAACGGCAGAGCGCTCGAGAGCTTTGCTACCGTCGA	342
Db	288	CATGCCAACCTTCTCTGTTTATGAGAGGAGAGAGCTCAAGACAGGGTTGTCGGAGCTAT	347
QY	343	CGAGGACGAGCTCCGGGACGCCGTCAAGGAAGTACGCCGCCG	384
Db	348	CAAGGAGGAGCTGACGACCAAGGTTGGGCTCCACGCGGCTGC	389

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 19:52:33 ; Search time 2102.06 Seconds
(without alignments)
9944.292 Million cell updates/sec

Title: US-10-005-429-13

Perfect score: 700
Sequence: 1 ggaaccacccaggaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em estba:*

2: em esthm:*

3: em estin:*

4: em estmu:*

5: em estov:*

6: em estpl:*

7: em estro:*

8: em htc:*

9: gb est1:*

10: gb est2:*

11: gb htc:*

12: gb est3:*

13: gb est4:*

14: gb est5:*

15: em estfun:*

16: em estom:*

17: em gss hum:*

18: em gss inv:*

19: em gss pln:*

20: em gss vrt:*

21: em gss fun:*

22: em gss nam:*

23: em gss mus:*

24: em gss pro:*

25: em gss rod:*

26: em gss phg:*

27: em gss vrl:*

28: gb gss1:*

29: gb gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	71.7	562	14	CF005608 QB113b03
2	497.6	71.1	568	14	CF020146 QB2b06.x
3	474.2	67.7	573	14	CF006552 QB120e10
4	458.4	65.5	503	14	CF019426 QB19c09

RESULT 1

CF005608

LOCUS

DEFINITION

CF005608

ACCESSION

CF005608.1

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF005608 562 bp mRNA linear EST 16-JUL-2003
QB113b03.xg QBI Zea mays cDNA clone QB113b03, mRNA sequence.

ALIGNMENTS

5	457.8	65.4	504	14	CF019475
6	452.4	64.6	496	14	CF007924
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9	411	58.7	430	14	CD972346
c 10	408	58.3	442	14	CD974597
c 11	393	56.1	411	14	CD976888
c 12	385.8	55.1	427	14	CF647253
c 13	380.4	54.3	400	14	CD974844
c 14	379	54.1	388	12	BG837010
c 15	376.6	53.8	426	14	CF008093
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c 20	344	49.1	737	14	CF006844
c 21	339.4	48.5	456	12	BG837151
c 22	337.8	48.3	359	14	CF008092
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c 24	243	34.7	1056	14	CA275558
c 25	233	33.3	519	14	CA273890
c 26	228.8	32.7	273	14	CD965475
c 27	225.8	32.3	316	14	CD949589
c 28	222.2	31.7	673	14	CA275630
c 29	217.8	31.1	681	28	BZ794456
c 30	207.2	29.6	600	14	CF041938
c 31	206.4	29.5	559	14	CD999290
c 32	206.2	29.5	544	9	AI621726
c 33	205.6	29.4	424	12	BI542528
c 34	205.6	29.4	459	14	CD651418
c 35	205.6	29.4	504	14	CF014883
c 36	205.6	29.4	513	14	CD996841
c 37	205.6	29.4	519	14	CD995652
c 38	205.6	29.4	523	14	CF042094
c 39	205.6	29.4	550	14	CF023788
c 40	205.6	29.4	553	9	AI438566
c 41	205.6	29.4	556	14	CD990879
c 42	205.6	29.4	560	9	AI621711
c 43	205.6	29.4	564	14	CB833972
c 44	205.6	29.4	564	14	CB885343
c 45	205.6	29.4	568	12	BM380699

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CF019553 QB11b06.x
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CD972346 QAE2e03.
CD974597 QAE4b02.
CD976888 QAF2b09.
CF647253 3530.1.41
CD974844 QAE50c02.
BG837010 Zm08.10f0
CF008093 QB17d05.x
CG158805 PUFV10TB
CC402188 PUFV10TB
CG323449 OGMFF20TV
CF006994 QB124f08.
CF006844 QB123c05.
BG837151 Zm08.06b0
CF008092 QB17d05.p
CA277200 SCACSD201
CA275558 SCBFSD103
CA273890 SCRLSD101
CD965475 SEK_153 G
CD949589 SAL_90 Ge
CA275630 SCBFSD103
BZ794456 PUGZ292TB
CF041938 QCI31112.
CD999290 QBF5c01.p
AI621726 486006H06
BI542528 949020H04
CD651418 3529.1.13
CF014883 QB119b04.
CD996841 QBC8e07.x
CD995652 QB2e06.y
CF042094 QCI33h12.
CF023788 QBS10h05.
AI438566 486006H06
CD990879 QAZ1f11.y
AI621711 486006F12
CB833972 3529.1.86
CB885343 3529.1.86
BM380699 MEST523-G

Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES
source

Location/Qualifiers
1..562
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/cultivar="F2"  
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/clone="QB113b03"  
/tissue_type="pedicel"  
/clone_lib="QB1"
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ORIGIN

[illegible]

RESISTANCE

CF020146 LOCUS 568 bp mRNA linear EST 17-JUL-2003
 DEFINITION QBN2b06.xg QBN Zea mays cDNA clone QBN2b06, mRNA sequence.
 ACCESSION CF020146
 VERSION CF020146.1 GI:32915334
 KEYWORDS EST.

SOURCE ORGANISM

Eukaryota, Viridiplantae; Streptophyta; Embryophyta, Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 568)
 Genoplate.
 Genoplate, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplate
 Genoplate
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplate' (<http://www.genoplate.com>
 and <http://genoplate-info.infobiogen.fr>).

FEATURES

```
Location/Qualifiers
1. .568
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QBN2b06"
/tissue_type="pedicel"
/clone_lib="QBN"
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ORIGIN

Query Match	71.1%	Score	497.6	DB	14	Length	568		
Best Local Similarity	97.2%	Misld. No.	1.9e-46						
Matches	529	Conservative	0	Predictions	9	Indels	6	Gaps	2

QY	1	GGATCCACACCCGAGGAAAGGAGACAGAGGGTTCGGAATAATGGCGCGCGAGGAGGGTGC	60
DB	25	GGATCCACACCCGAGGAAAGGAGACAGAGGGTTCGGAATAATGGCGCGCGAGGAGGGTGC	84
QY	61	CGTGATCGCGTGCACACACACACAGGACAGATTCCACGCCCGCCATGGCCACAGGCCCAAGAGCA	120
DB	85	CGTGATCGCGTGCACACACACAGGACAGATTCCACGCCCGCCATGGCCCAAGGCCCAAGAGCA	144
QY	121	GGCGAAGCTGGTGGTTCATCGAC-----TTCATGGCCCCCTGGTGCAGTGGGTGCCAGATGA	176
DB	145	GGCGAAGCTGGTGGTTCATCGACTTCGTTTCATGGCCCCCTGGTGGTGGTGGTGCAGATGA	204
QY	177	TGGCCCCGGTGTACGGCGATCGCGCAGCAAGTACCTTCGCGCGTCTCTCTCGAGGTCG	236
DB	205	TGGCCCCGGTGTACGGCGATCGCGCAGCAAGTACCTCTCCGCGTCTCTCTCGAGGTCG	264
QY	237	ACGTCGACGAACCTCTCGGAAGTCGGAAGATCTACGGGCTCCATCGTGAATGCCACCTTCT	296
DB	265	ACGTCGACGAACCTCTCGGAAGTCGGAAGATCTACGGGCTCCATCGTGAATGCCACCTTCT	324
QY	297	GCTTCATCAGAAACGGCGAGACGCTCGAGAGCTTTTGCTACCGTCCACGAGGACGAGTCC	356
DB	325	GCTTCATCAGAAACGGCGAGACGCTCGAGAGCTTTTGCTACCGTCCACGAGGACGAGTCC	384
QY	357	GGGAGCGCGTCAGGAAGTACGCGCGCGCTGGCACTACGACGGCTCTCTCGCTCGGGGTCG	416
DB	385	GGGAGCGCGTCAGGAAGTACGCGCGCGCTGGCACTACGACGGCTCTCTCGCTCGGGGTCG	444
QY	417	CCTAATTCAGGAGATGTGATGTGTAGCAATAAGCGCGCGCGC--ACCAAGTCGTCAATAAA	474
DB	445	CCTAATTCAGGAGATGTGATGTGTAGCAATAAGCGCGCGCGCTCGTCAATAATAAA	504
QY	475	TAATAATAATAATAATAATAATAATAATAATAATAAGGCCAAAGCTACGACGACAAA	534
DB	505	TAATAATAATAATAATAATAATAATAATAATAATAAGGCCAAAGCTACGACGACAAA	564
QY	535	TTAG 538	
DB	565	TTAG 568	

RESULT 3

CF006552	573 bp	mRNA	linear	EST 16-JUL-20003
LOCUS				
DEFINITION	QBI120e10.xg	QBI	Zea mays	CDNA clone QBI20e10, mRNA sequence.
ACCESSION	CF006552			
VERSION	CF006552.1	GI:	32866870	
KEYWORDS	EST.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
	Eukaryota;	Viridiplantae;	Streptophyta;	Embryophyta; Tracheophyta;
	Spermatophyta;	Magnoliophyta;	Liliopsida;	Poales; Poaceae; PACCAD
	clade; Panicoideae;	Andropogoneae;	Zea.	
REFERENCE	1 (bases 1 to 573)			
AUTHORS	Genoplaute.			
TITLE	Genoplaute, a major partnership french program in plant genomics			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Genoplaute			


```

REFERENCE
AUTHORS
TITLE
Genoplatte, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)
COMMENT
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.infobiogen.fr).

FEATURES
source
1..496
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QB16a01"
/tissue_type="pedicel"
/clone_lib="ORI"

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Query Match	64.6%;	Score 452.4;	DB 14;	Length 496;
Best Local Similarity	98.9%;	Pred. No. 2.1e-41;		
Matches 467;	Conservative 0;	Mismatches 1;	Indels 4;	Gaps 1;
1	GGATCCACACCGAGGAAAGGAGACAGAGGGTCCGAATAATGGCGCGCGAGGAGGGTGC	60		
25	GGATCCACACCGAGGAAAGGAGAGAGGGTCGGAATATGGCGCGCGAGGAGGGTGC	84		
61	CGTGATCGGTGCCACACACAGGACGAGTTGACGCCCGCGCATGGCCAAAGGCCAAGAGCA	120		
85	CGTGATCGGTGCCACACCAAGGACGAGTTGACGCCCGCGCATGGCCAAAGGCCAAGAGCA	144		
121	GGGCAAGCTGGTGGTTCATCGAC-----TTCATGGCCCCCTGGTGCAGTGGGTGCCAGATGA	176		
145	GGGCAAGCTGGTGGTTCATCGACTTCGTTTCATGGCCCCCTGGTGCAGTGGGTGCCAGATGA	204		
177	TGGCCCGGTGTACGGCGACTCGGCCACGACGATCCCTTCGCGGCTCTTCCTCGAGGTGC	236		
205	TGGCCCGGTGTACGGCGACTCGGCCACGACGATCCCTTCGCGGCTCTTCCTCGAGGTGC	264		
237	ACGTGACGAACCTGTGGAACTGCGGAAGATCTACGGCGTCCATGTGATGCGCACTTCT	296		
265	ACGTGACGAACCTGTGGAACTGCGGAAGATCTACGGCGTCCATGTGATGCGCACTTCT	324		
297	GCTTTCATCAGGAACGGCGAGAGCTCGAGAGCTTTGTTCACGTCGACGAGGACGAGTCC	356		
325	GCTTTCATCAGGAACGGCGAGAGCTTCGAGAGCTTTGTTCACGTCGACGAGGACGAGTCC	384		
357	GGAGACGGCTCAGGAAGTACGCGCGCGCTGGGACATACGAGGGCTCCTCGCGGTCCG	416		
385	GGAGACGGCTCAGGAAGTACGCGCGCGCTGGGACATACGAGGGCTCCTCGCGGTCCG	444		
417	CCTAAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGACCAAGCTCGTC	468		
445	CCTAAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGACCAAGCTCGCC	496		

RESULT 7	CF019553	503 bp	linear	EST 17-JUL-2003
	CF019553	QBN1h06.xg	QBN	Zea mays cDNA clone QBN1h06, mRNA sequence.
	CF019553			
	CF019553.1	GI:32914741		
	EST.			
	KEYWORDS			
	SOURCE			
	Zea mays			
	ORGANISM			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.			
	REFERENCE			
	1 (bases 1 to 503)			

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1.480
source
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="R2"
/db_xref="taxon:4577"
/clone="QA6f04"
/tissue_type="pericarp"
/clone_lib="QA6"

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Query Match	63.9%;	Score 447;	DB 14;	Length 480;		
Best Local Similarity	99.1%;	Pred. No. 8.4e-41;				
Matches 461;	Conservative	0;	Mismatches	0; Indels	4; Gaps	1;
54	AGGGTGC CGTGTATCGGTCGCCACACCAAGACGAGTTTCGACGCGCCGATGGCCAAAGGCCA	113				
1	AGGGTGC CGTGTATCGGTCGCCACACCAAGACGAGTTTCGACGCGCCGATGGCCAAAGGCCA	60				
114	AGGACGAGGCGAAGCTGGTGGTTCATCGAC-----TTTCATGGCCCCCTTGGTGCAGTGGGTGC	169				
61	AGGACGAGGCGAAGCTGGTGGTTCATCGACTTCCTGTTTCATGGCCCCCTTGGTGCAGTGGGTGC	120				
170	CAGATGATGGCCCCCGGTGTACGGGACTCGCCAGCAAGTACCTCTTCGGGGTCTTCTCTC	229				
121	CAGATGATGGCCCCCGGTGTACGGGACTCGCCAGCAAGTACCTCTTCGGGGTCTTCTCTC	180				
230	GAGGTGCACTGCACGAACTGCTGGAAGTCCGGAAGATCTACGGGTCTCATGTGATGCCG	289				
181	GAGGTGCACTGCACGAACTGCTGGAAGTCCGGAAGATCTACGGGTCTCATGTGATGCCG	240				
290	ACCTTCTCGTTCATCAGGAACCGCGAGACGCTCGAGAGCTTTGCTACCGTCCGACGAGAC	349				
241	ACCTTCTCGTTCATCAGGAACCGCGAGACGCTCGAGAGCTTTGCTACCGTCCGACGAGAC	300				
350	GAGTCCCGGACCGCGTCAGGAAGTACGCGCGCGCTGGCACTACGACGGCTCTCGCTCG	409				
301	GAGTCCCGGACCGCGTCAGGAAGTACGCGCGCGCTGGCACTACGACGGCTCTCGCTCG	360				
410	GGTCCGCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGACCACTAGTCTCA	469				
361	GGTCCGCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGACCACTAGTCTCA	420				
470	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	514				
421	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	465				

CD9723346	CD9723346	430 bp	mRNA	linear	EST 16-JUL-2003
LOCUS	QAE320e03.yg	QAE Zea mays	CDNA clone	QAE20e03	mRNA sequence.
DEFINITION	CD9723346				
ACCESSION	CD9723346				
VERSION	CD9723346.1	GI:32832668			
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 430)				
GENEPLANTE.	Genoplante.				
TITLE	Genoplante, a major partnership french program in plant genomics				

JOURNAL
COMMENT

Unpublished (2003)
Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.inbioigen.fr).

FEATURES
source

Location/Qualifiers
1. 430
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QAE20e03"
/tissue_type="pericarp"
/clone_lib="QAE"

ORIGIN

Query Match 58.7%; Score 411; DB 14; Length 430;
Best Local Similarity 99.1%; Pred. No. 8.7e-37;
Matches 425; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 54 AGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCATGGCCCAAGGCCA 113
DB 1 AGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCATGGCCCAAGGCCA 60
QY 114 AGGACAGGCGCAAGCTGGTGTGATCGAC-----TTATGCGCCCTGCTGCAAGTGGTGC 169
DB 61 AGGACAGGCGCAAGCTGGTGTGATCGAC-----TTATGCGCCCTGCTGCAAGTGGTGC 120
QY 170 CAGATGATGCGCCCGGTGTCAGCGGAGCTGCGCAGCAAGTACCTTTCCGCGGCTTTCTTC 229
DB 121 CAGATGATGCGCCCGGTGTCAGCGGAGCTGCGCAGCAAGTACCTTTCCGCGGCTTTCTTC 180
QY 230 GAGGTGCACTCGACAGCAACTGCTGGAAGTCCGCAAGATCTACGGCTCCATGTGATCCCG 289
DB 181 GAGGTGCACTCGACAGCAACTGCTGGAAGTCCGCAAGATCTACGGCTCCATGTGATCCCG 240
QY 290 ACCTTCGCTTCATCAGCAAGCGCGAGACGCTCGAGAGCTTTGCTACCGTCGACGAGGAC 349
DB 241 ACCTTCGCTTCATCAGCAAGCGCGAGACGCTCGAGAGCTTTGCTACCGTCGACGAGGAC 300
QY 350 GAGTCGCGGACGCGCTCAGCAAGTACGCGCGCTGCGCACTACGAGGCTTCGCTCG 409
DB 301 GAGTCGCGGACGCGCTCAGCAAGTACGCGCGCTGCGCACTACGAGGCTTCGCTCG 360
QY 410 GCGTCGCGCTTAATTCAGGAGATGTGTGAGCAATAGCGCGCGGACCACTAGTCTCA 469
DB 361 GCGTCGCGCTTAATTCAGGAGATGTGTGAGCAATAGCGCGCGGACCACTAGTCTCA 420
QY 470 ATAAATAAA 478
DB 421 ATAAATAAA 429

RESULT 10
CD974597/c

LOCUS
DEFINITION
QAE48b02.yg QAE Zea mays cDNA clone QAE48b02, mRNA sequence.
ACCESSION
CD974597
VERSION
CD974597.1 GI:32834919
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 442)
REFERENCE
AUTHORS
TITLE
Genoplatte, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)

COMMENT

Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com
and http://genoplatte-info.inbioigen.fr).

FEATURES
source

Location/Qualifiers
1. 442
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QAE48b02"
/tissue_type="pericarp"
/clone_lib="QAE"

ORIGIN

Query Match 58.3%; Score 408; DB 14; Length 442;
Best Local Similarity 97.9%; Pred. No. 1.8e-36;
Matches 425; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
QY 42 TGGCGCGCGAGGAGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCA 101
DB 434 TGGCGCGCGAGGAGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCA 375
QY 102 TGGCGCGCGCGAGGAGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCA 157
DB 374 TGGCGCGCGCGAGGAGGTCGCGTGATCGGTGCGCCACCAAGGACGAGTTGCAAGCCCGCA 315
QY 158 TCGAGTGGTGGTCAGATGATGCGCGCGGTGACGCGGAGCTGCGCAGCAAGTACCTTCC 217
DB 314 TCGAGTGGTGGTCAGATGATGCGCGCGGTGACGCGGAGCTGCGCAGCAAGTACCTTCC 255
QY 218 GCGGCTTCTCTCGAGGTGCACTCGACGAACTGCTGGAAGTCCGGAAGATCTACGCGCTC 277
DB 254 GCGGCTTCTCTCGAGGTGCACTCGACGAACTGCTGGAAGTCCGGAAGATCTACGCGCTC 195
QY 278 CATGTGATGCGCACTCTCTGCTTCATCAGGACGCGGAGCGCTCGAGAGCTTTGCTACC 337
DB 194 CATGTGATGCGCACTCTCTGCTTCATCAGGAAACGCGGAGCGCTCGAGAGCTTTGCTACC 135
QY 338 GTCGACGAGGACGAGCTCCGCGACGCGCTCAGCAAGTACGCGCGCTGCGCACTACGAG 397
DB 134 GTCGACGAGGACGAGCTCCGCGACGCGCTCAGCAAGTACGCGCGCTGCGCACTACGAG 75
QY 398 GTCCTCGCTCGCGCTCGCGCTTAATTCAGGAGATGTGTGAGCAATAGCGCGCGCG 457
DB 74 GTCCTCGCTCGCGCTCGCGCTTAATTCAGGAGATGTGTGAGCAATAGCGCGCGCG 15
QY 458 CACCGTCTGCTCAAT 471
DB 14 CACCGTCTGCTCAAT 1

RESULT 11
CD976888

LOCUS
DEFINITION
QAF23b09.yg QAF Zea mays cDNA clone QAF23b09, mRNA sequence.
ACCESSION
CD976888
VERSION
CD976888.1 GI:32837210
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 411)
REFERENCE
AUTHORS
TITLE
Genoplatte, a major partnership french program in plant genomics
JOURNAL
Unpublished (2003)
COMMENT
Contact: Genoplatte

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source
1. 411
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QAF23b09"
/tissue_type="pericarp"
/clone_lib="QAF"

ORIGIN

Query Match 56.1%; Score 393; DB 14; Length 411;
Best Local Similarity 99.0%; Pred. No. 8.8e-35;
Matches 407; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
Qy 54 AGGTTGGCGTATCGGTGGCCACACCAAGGACGAGTTGCGACGCCCGCATGGCCCAAGGCCA 113
Db 1 AGGTTGGCGTATCGGTGGCCACACCAAGGACGAGTTGCGACGCCCGCATGGCCCAAGGCCA 60
Qy 114 AGGAGCAGGCGAGCTGGTGTCTATCGAC---TTCTATGCGCCCGCTGGTGGTGGTGC 169
Db 61 AGGAGCAGGCGAGCTGGTGTCTATCGAC---TTCTATGCGCCCGCTGGTGGTGGTGC 120
Qy 170 CAGATGATGCCCCCGGTGTACGGGAGCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 229
Db 121 CAGATGATGCCCCCGGTGTACGGGAGCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 180
Qy 230 GAGTTCAGCTGACGAGTCTGGAAGTCGCGAGTCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 289
Db 181 GAGTTCAGCTGACGAGTCTGGAAGTCGCGAGTCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 240
Qy 290 ACCTTCTGCTTCAATGAGAACGCGAGACCTCTGAGAGCTTTTCTACCTCGACGAGGAC 349
Db 241 ACCTTCTGCTTCAATGAGAACGCGAGACCTCTGAGAGCTTTTCTACCTCGACGAGGAC 300
Qy 350 GAGTTCGCGGACGCGTACGAGTACGCGCGCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 409
Db 301 GAGTTCGCGGACGCGTACGAGTACGCGCGCTGCGGACGAGTACCTTTCCGGGTCTTCCTC 360
Qy 410 GGTTCGCTTAATTCAGGAGATGTGTGTAGCAAAATAGCGCGCGCAC 460
Db 361 GGTTCGCTTAATTCAGGAGATGTGTGTAGCAAAATAGCGCGCGCAC 411

RESULT 12

CF647253
LOCUS 427 bp mRNA linear EST 02-OCT-2003
DEFINITION 3530.1_41.1_D03.x.1 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
CF647253
ACCESSION
VERSION CF647253.1 GI:37419153
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 427)
Walbot V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1_41.1 row: D column: 03.
Location/Qualifiers
1. 427
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"

FEATURES

source

Invitrogen from multiple tissues"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/note="Organ: silks, husks, ears, pollen, shoot tips.
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSPORT vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 day aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; all
leaves with an expanded or partially expanded sheath
were removed; 8. mature leaf tissue; 9. 0.5 cm long root
tips from 15 day old seedlings; 10. 10 day whole seed; 11.
12 day endosperm and embryo; 12. 17 day endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
unigene clones from the Maize Gene Discovery EST
sequencing projects. Clones can be ordered through the
ZmDB web site or directly from the University of Arizona
(<http://www.genome.arizona.edu/orders/>). High density
filters containing over 18,000 clones can also be ordered
from the University of Arizona."

ORIGIN

Query Match 55.1%; Score 385.8; DB 14; Length 427;
Best Local Similarity 98.3%; Pred. No. 5.4e-34;
Matches 401; Conservative 0; Mismatches 3; Indels 4; Gaps 1;
Qy 1 GGATCCACACCCGAGGAAGGAGAAGA---GAGGGTGGGAATAATGGCGCGGAGGAGG 56
Db 20 GGATCCACACCCGAGGAAGGAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 79
Qy 57 GTGCCGCTGATCGGTGCTCCACCAAGGAGGAGTTCACGCCCGCATGGCCAGGCCAAGG 116
Db 80 GTGCCGCTGATCGGTGCTCCACCAAGGAGAGGTTCACGCCCGCATGGCCAGGCCAAGG 139
Qy 117 AGCAGGCGAAGCTGGTGGTTCATCGACTTCATGCCCGCCCTGGTGCAGTGGTCCAGATCA 176
Db 140 AGCAGGCGAAGCTGGTGGTTCATCGACTTCATGCCCGCCCTGGTGGTGGTCCAGATCA 199
Qy 177 TGGCCCCGGGTACCGCGGACTGCGCGCAGCAAGTACCTTCCCGGGTCTTCCCTCGAGTGC 236
Db 200 TGGCCCCGGGTACCGCGGACTGCGCGCAGCAAGTACCTTCCCGGGTCTTCCCTCGAGTGC 259
Qy 237 ACCTGCGAAGAACTGCTGGAAGTCGGAAGATCTACGGCGTCCATGTGATGATCGCGACTTCT 296
Db 260 ACCTGCGAAGAACTGCTGGAAGTCGGAAGATCTACGGCGTCCATGTGATGATGATCGCGACTTCT 319

[illegible]

RESULT 13	CD974844/c	CD974844	400 bp	mRNA	linear	EST 16-JUL-2003
LOCUS	CD974844					
DEFINITION	QAE50C02.yg	QAE	Zea mays	cdna clone	QAE50c02	mRNA sequence.
ACCESSION	CD974844					
VERSION	CD974844.1	GI:32835165				
KEYWORDS	EST.					
SOURCE	Zea mays					
ORGANISM	Zea mays					

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 400)

REFERENCE
1 (bases 1 to 400)
Genopante; *Genopante*; *Genopante*.
Genopante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genopante

Genopliance
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

```

FEATURES
source
1. 400
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="P2"
/db_xref="taxon:4577"
/clone="QA550C02"
/tissue_type="pericarp"
/clone_lib="OAS"

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Query Match 54.3%; Score 380.4; DB 14; Length 400;
Best Local Similarity 98.8%; Pred. No. 2.2e-33;
Matches 395; Conservative 0; Mismatches 1; Indels 4;

Qy

76 CACCAAGGACGAGTTGGACGCCCGCCATGGCCAAGSCCAGGAGCACGGGCAGCTGGTGT 135
|||||
|||

Dd

400 CACCAAGGACGAGTTGGACGCCCGCCATGGCCAAGSCCAGGAGCACGGGCAGCTGGTGT 341
|||||
|||

Qy 136 CATCGAC---TTTCATGCCCCCTGGTGCAGTGGGTGCCAGATGATGCCCCCGGTGTACG 191

Db 340 CATCGACTTGTTTCATGCCCCCTGGTGCAGTGGGTGCCAGATGATGCCCCCGGTGTACG 281

[illegible]

252 TGGAAATCGCGAAGATCTACGGGCTCCATGTGTGCGGACCTTCTGCTTCATCAGGAACG 311

Db 220 TGGAGTCGCGAAGATCTACGGGCTCCATGTGATCGCAGCTTTTGCTTCATCAGGAACG 161

Qy 312 GCGAGACGCTCGAGAGCTTTTGCTACCTCGA CGAGGACGAGCTCCGGGACGCCGTCAGGA 371

Db	160	GCEAGACGCTCGAGAGCTTTGCTACCGTCGACGAGGACGAGCTCCGGGACGCCGTCAGGA	101
Qy	372	AGTACGGCGCGCTGGGCACTACGACGGCTCTGCTCGGGGTCCGCTCAATTTCAGGAGAT	431

Db 100 AGTACGCGCGCTGGCACTACGACGGCTCCTGCCTCGCGTCCGCTAATTCAGGAGAT 41

Qy 432 GTGATGTGTAGCAAAATAGCGCGCGCGCACCAAGTCGTCAAT 471

D_b 40 GTGATGTGTAGCAATAGCGCGCGCACCGTGTCAAT 1

RESULT 14	LOCUS	DEFINITION
BG837010/c		

EG837010 388 bp mRNA linear EST 25-MAY-2001
Zm08 10f04 A
Zm08_AAF_C4CORC_Fusarium graminearum inoculated corn ear Zea mays
cDNA clone Zm08 10f04, mRNA sequence.

CGAR CIGRUE 480607-1010107
ACCESSION BG837010
VERSION BG837010.1 GI:14203333
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCES

Moors, A., Hattori, J. I., Ouellet, T., Robert, L. S., Singh, J. A., Spratt, D. and Tinker, N. A.

TITLE	JOURNAL
Expressed Sequence Tags from Developing Maize Kernels Six Days after Silk Channel Inoculation with <i>Fusarium graminearum</i>	Unpublished (2001)

COMMENT

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA

Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrisj@em.a

FEATURES	Location/Qualifiers
source	1. .388

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/organism="Zea mays"
/moi_type="mRNA"
/cultivar="CO430"
/db_xref="taxon:4577"
/cions="Zm08_10r04"
/issue_type="developing kernels (sibcrossed)"
/dev_stage="10-11 days post-silk emergence"
/clone_lib="Zm08_AAFc_ECORC_Fusarium_graminearum_inoculate
d corn ear"

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ORIGIN

Query Match	54.1%	Score 379;	DB 12;	Length 388;
Best Local Similarity	98.7%;	pred. NO. 3.2E-33;		
Matches 382;	Conservative	0;	Mismatches 5;	Indels 0;
				Gaps 0;

Qy	62	GTGATCGGTGCGCCACCAAGGA	CGAGTTTCGACGCCCGCATGGCC	AAGGCCAAGGCAG	121
Db	387	GTGATCGGTGCGCCATCCAAAGGA	CGAGTTTCGACGCCCGCATGGCC	AAGGCCAAGGCAG	328

Qy	122	GGCAAGCTGGTGGTCATCGACTTCATGGCCCCCTCGTGCAGTGGGCCAGATGATGGCC	181
nb	327	GGCAAGCTGGTGGTCATCGACTTCATGGCCCCCTCGTGCAGTGGGCCAGATGATGGCC	268

Qy 182 CGCGTGTA CGCGGACTCGCGCAGCAAGTACCGCTTCGCGGCTCTTCCTCGAGGTGAGGTC 241

DB	267	CCGCGTGTACCGCGACTCGCGCAGCAAGTACCTCTCCGCGGTCTTCTCTCGAGGTCGACGTC	208
QY	242	GACGAACTGCTGGAAGTCGCGAAGATCTACGGCGTCCATGTGATGSCGACCTTCGCTTC	301

Db	207	GAGCAACTGCTGGAAAGTCGCGAAGATCTACGGCGTCCATGTGATGCCGACCTTCTGCTTC	148
Qy	302	ATCAGGAACGGGAGAACGCTCGAGAGCTTTGCTACCGTCGACGAGGACGAGCTCCGGGAC	361

28	71	10.1	255	4	US-09-621-976-9A06	Sequence 9406, Ap
29	71	10.1	1725	4	US-09-668-057A-21	Sequence 21, Appl
30	70.4	10.1	2186	4	US-09-360-545-66	Sequence 66, Appl
31	70.4	10.1	10288	4	US-09-845-917A-28	Sequence 28, Appl
32	70.4	10.1	13414	4	US-09-845-917A-27	Sequence 27, Appl
33	70.2	10.0	1008	4	US-09-780-641-1	Sequence 1, Appl
34	70	10.0	183	4	US-09-621-976-13606	Sequence 13606, A
35	69.6	9.9	1582	3	US-08-545-196B-10	Sequence 10, Appl
36	69.6	9.9	1582	3	US-08-545-196B-12	Sequence 12, Appl
37	68.2	9.9	2550	6	5358287-23	Patent No. 5258287
38	68.8	9.8	1602	1	US-08-530-950-3	Sequence 3, Appl
39	68.8	9.8	1602	3	US-08-888-429A-3	Sequence 3, Appl
40	68.8	9.8	1602	3	US-09-149-879-3	Sequence 3, Appl
41	68.8	9.8	1602	4	US-09-057-009-3	Sequence 3, Appl
42	68.8	9.8	1602	4	US-09-593-653-3	Sequence 3, Appl
43	68.8	9.8	8100	4	US-09-554-337-4	Sequence 4, Appl
44	68.8	9.8	11517	3	US-07-920-281C-1	Sequence 1, Appl
45	68.8	9.8	11517	3	US-08-466-277-1	Sequence 1, Appl

39	68.8	9.8	1602	3	US-08-888-429A-3	Sequence 3, Appl
40	68.8	9.8	1602	3	US-09-149-879-3	Sequence 3, Appl
41	68.8	9.8	1602	4	US-09-057-009-3	Sequence 3, Appl
42	68.8	9.8	1602	4	US-09-593-653-3	Sequence 3, Appl
43	68.8	9.8	8100	4	US-09-554-33-4	Sequence 4, Appl
44	68.8	9.8	11517	1	US-07-920-281C-1	Sequence 1, Appl
45	68.8	9.8	11517	3	US-08-466-277-1	Sequence 1, Appl

```

RESULT 1
US-09-621-976-1844
; Sequence 1844, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335

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: SEQ ID NO 1844
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: LENGTH: 466
:
: TYPE: DNA
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FEATURE:
; NAME/KEY: CDS
; LOCATION: 71..256
; NAME/KEY: s19_peptide
; LOCATION: 71..199
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.30000019073486
; OTHER INFORMATION: seg VVIDETAACWCHA/AF
US-09-621-976-1844

Query Match          27.9%; Score 195.2; DB 4; Length 466;
Best Local Similarity 72.0%; Pred.No.3.e-31;
Matches 268; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

QY      36  GAATATGGCGGCGGAGGAGGGTGCGGTGATCGGTGCCACACCAAGGACGAGTTTCGACG 95
Db      66  GATCAATGGCGTCCGAGCAGGGAGTGTGATCGGTGCCACACGACGAGGCTGAGTTTCGACG 125

QY      96  CCGCATGGCCCAAGCCCAAGGAGGAGGCAAGCTGGTGGTCACTGCACATTCATGGCCCCCCT 155
Db      126  CCCACATGACCAAGGCCCCAGAGCGGCGCAAGCTGGTGGTCACTGCACATTCATGGCGCCT 185

QY      156  GGTGCAGTGGGFGCCAGATGATGGGCCCGGGTGTATGCGGACATGGCGCCACGATGCCCTT 215
Db      186  GGTGC-GTCCATGCGCGGCGCATCGGCCCACTGTTGTGCAACACGCGCAAGATTCACATC 244

QY      216  CGCGGGTCTTCTTCGAGGTTCGACGTGACGAACTGTGGAAGTGCGGAAGATCTACGGCG 275
Db      245  AGTGGTCTTCTTCGAGGTGAGGTGACGAAAGTGAAGAGTCAACCGCGGCCCTACGAGG 304

QY      276  TCCATGTGATGCCGACCTTCTCGCTTCATCAGGAACGGCGAGACGCTTCGAGAGCTTTGCTA 335

```

RESULT 3
US-09-540-014-3
Sequence 3, Application US/09540014
Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaux, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Raviex Gene f

Patent No. 6380372
GENERAL INFORMATION:
APPLICANT: Cho, Myeong-Je
APPLICANT: Del Val, Greg
APPLICANT: Caillaud, Maxime
APPLICANT: Lemaun, Peggy G.
APPLICANT: Euchanau, Bob E.
TITLE OF INVENTION: Barley Gene for Thioredoxin and
TITLE OF INVENTION: NADP-Thioredoxin Reductase
FILE REFERENCE: 2001-0701-30
CURRENT APPLICATION NUMBER: US/09/540,014
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 60/127,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US 60/169,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 60/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,739

Query Match 16.9%; Score 118; DB 4; Length 369;
Best Local Similarity 59.1%; Pred. No. 1.5e-15;
Matches 202; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 43 GCGCGCCGAGGAGGTCGCGTGATCGCGTCCACCAAGGACGAGTTCCAGCGCCCGCAT 102
DB 21 GCGCGCAGTGGCGCGGAGGTGATCTCGTCCACAGCTGGAGCAGTGACATCCAGAT 80
QY 103 GCGCAAGCCCAAGAGGAGGCGGAGCTGGTGTGATCATGCTTATGCGCCCGCTGTCAG 162
DB 81 CGAGGAGGCCCAACACCGCCCAAGAGCTGGTGGTGAITGACTTCACTCATGCTGTCGG 140
QY 163 TGGGTGCAGATGATGCCCGCGGTGTACGGGACTGGCGCCAGCAAGTACCTTCCGCGGT 222
DB 141 ACCATGCGCATCATGCTCCAGTTTCGCTGATCTCGCAAGAGTTCCCAATGCTGT 200
QY 223 CTTCCTCGAGGTGACGTGACGAACTGCTGGAAGTCCGGAAGATCTACGCGTCCATGT 282
DB 201 TTTCCTCAAGTCCAGCTGAGTGAATCAAGCCCAITGCTGAGCAATTCAGTGTGAGGC 260
QY 283 GATCGCGACCTTCGCTTCATCAGGACGGCGAGAGCTCGAGAGCTTTGCTACCGTCCA 342
DB 261 CATGCCAACGTTCTGTTTCATGAAGAGGAGAGCTCAAGACAGGGTTGTCGGAGCTAT 320
QY 343 CGAGGACGAGCTCCGGGAGCGCGTCAGGAAAGTACGCGCGCGC 384
DB 321 CAAGGAGGAGCTGACCGCCAGGTTGGGCTTCACGCGCGCGC 362

RESULT 6
US-09-313-294A-5840
; Sequence 5840, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313.294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 5840
; LENGTH: 278
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700350762H1
; NAME/KEY: unsure
; LOCATION: 275
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5840

Query Match 16.2%; Score 113.6; DB 4; Length 278;
Best Local Similarity 71.6%; Pred. No. 1.1e-14;
Matches 149; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCGAGGAGGTCGCGTGATCGCGTCCACCAAGGACGAGTTCCAGC 95
DB 41 GATCAATGCGCTCCGAGCAGGAGTCTGTGATCGCGTCCACAGCAAGGCTGAGTCCAGC 100
QY 96 CCGCATGCGCCCAAGCCCAAGCAGGAGCTGGTGTGATCATGCTTATGCGCCCGCT 155
DB 101 CCCATGACCAAGGCCCAAGAGCCCGGAGCTGGTGTGATCATGCTTATGCGCGCT 160
QY 156 GGTGAGTGGGTGCCAGATGATGCGCCCGGTGTGATGCGGAGTGGCCAGCAAGTACCTT 215
DB 161 GGTGCGGTCCATGCGCGCCATGCGCCCATGTCGACATGTTGTTGGAACACGCAAGAAATTCATTC 220
QY 216 CCGCGGTCTTCTCGAGGTTCAGCTCCA 243

PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: wheat thioredoxin h cDNA
US-09-540-014-5

Query Match 17.1%; Score 119.6; DB 4; Length 393;
Best Local Similarity 59.4%; Pred. No. 7.4e-16;
Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 43 GCGCGCCGAGGAGGTCGCGTGATCGCGTCCACCAAGGACGAGTTCCAGCGCCCGCAT 102
DB 48 GCGCGTGGCGCGGAGGTGATCTCGTCCACAGCTGGAGCAGTGACATCCAGAT 107
QY 103 GCGCAAGCCCAAGAGGAGGCGGAGCTGGTGTGATCATGCTTATGCGCCCGCTGTCAG 162
DB 108 CGAGGAGGCCCAACCGCCCAAGAGCTGGTGGTGAITGACTTCACTCATGCTGTCGG 167
QY 163 TGGGTGCAGATGATGCCCGCGGTGTACGGGACTGGCGCCAGCAAGTACCTTCCGCGGT 222
DB 168 ACCATGCGCATCATGCTCCAGTTTCGCTGATCTCGCAAGAGTTCCCAAGTGTGT 227
QY 223 CTTCCTCGAGGTGACGTGACGAACTGCTGGAAGTCCGGAAGATCTACGCGTCCATGT 282
DB 228 TTTCCTCAAGTCCAGCTGATGATGAAGCCCAITGCTGAGCAATTCAGCGTCCAGGC 287
QY 283 GATCGCGACCTTCGCTTCATCAGGACGGCGAGAGCTCGAGAGCTTTGCTACCGTCCA 342
DB 288 CATGCCAACCTTCGTTTCATGAAGAGGAGAGCTCAAGACAGGGTTGTCGGAGCTAT 347
QY 343 CGAGGACGAGCTCCGGGAGCGCGTCAGGAAAGTACGCGCGCGC 384
DB 348 CAAGGAGGAGCTGACCAAGGTTGGGCTTCACGCGCGCTGC 389

RESULT 5
US-09-540-014-1
; Sequence 1, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioredoxin and
; FILE REFERENCE: NADP-Thioredoxin Reductase
; CURRENT APPLICATION NUMBER: US/09/540.014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: barley thioredoxin h cDNA
US-09-540-014-1

RESULT 7

US-08-181-271A-103

; Sequence 103, Application US/08181271A

; Patent No. 5614395

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

; APPLICANT: Harms, Christian

; APPLICANT: Meins, Jr., Frederick

; APPLICANT: Montoya, Alice

; APPLICANT: Moyer, Mary B.

; APPLICANT: Neuhaus, Jean-Marc

; APPLICANT: Payne, George B.

; APPLICANT: Sperison, Christoph

; APPLICANT: Stinson, Jeffrey R.

; APPLICANT: Umes, Scott J.

; APPLICANT: Ward, Eric R.

; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/181.271A

; FILING DATE: 13-JAN-94

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/093,301

; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/937,197

; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/678,378

; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/305,566

; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/165,667

; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/042,847

; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/632,441

; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/425,504

; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/848,506

; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-181-271A-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;

Best Local Similarity 54.4%; Pred. No. 2.7e-09;

Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

QY 48 CCGAGGAGGGTCCCGTGAFCGGTGGCCACCAAGACGAGTTCGACGCCCGCCATGGCCA 107

Db 73 CCGAGGAGGGACAGTGTTCGGCTGCCACAGGTTGAGGAATGGAACGAGTACTTCAAGA 132

QY 108 AGCCCAAGCAGCAGGGCAGCTGTGTCTATCATGCTTTCATGCCCGCCCTGGTTCAGTGGGT 167

Db 133 AAGCGCTTGAGACTAAGAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 192

QY 168 GCCAGATGATGGCCCGCGGTGTACGGGACTTGGCCGACGAACTTCCCTTCGGCGGTCTTC 227

Db 193 GCGTTTATTTGCCCCCAATTTCTGTGACATGCTAAAGAGATGCCCATGTTATATTC 252

QY 228 TCGAGTTCAGCTCGACGAACTGCTGGAAGTCGC-GAAGATCTACGGCTCCATGTGTATG 286

Db 253 TCAAGGTTGATGTTGATGAAGTGAAGCTGTTTTCAGCGGGAATGGAGTGTGGAGGCAATG 312

QY 287 CCGACCTTCTCTTCATCAGGAACCGCGAGACGCTCGAGAGCTTTCTACCGTCGACGAG 346

Db 313 CCAACTTTTGTCTTTCATTAAGATGGAAGAAAGTGGACAGAGTTGTTGTTGCCAAGAAA 372

QY 347 GACGAGCTCGGAGCGCCCTCAGGAAGTACGGCGCTGCGGCTGGCAGTACGACGCTCCTGCC 406

Db 373 GAGGAGTTGACGACGACCATAGTGAAGCATGCTGCTCTCTCTACTGTCTACTGTGAATC 432

QY 407 TC 408

Db 433 TC 434

RESULT 8

US-08-449-315-103

; Sequence 103, Application US/08449315

; Patent No. 5650505

; GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.

APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christopher
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Utnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USSES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA: US 07/305,566
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA: US 08/042,847
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA: US 07/425,504
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA: US 07/768,122
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA: US 07/368,672
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rimer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-449-315-103
Query Match 12.5% Score 87.6; DB 1; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-09;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;
QY 48 CCGAGGAGGGTGGCGTGCATCGCGTGCACACCAAGGACGAGTTCGACGCCCGCATGSCCA 107
Db CCGAGGAGGGGCAAGTGTTCGGGTGCCCAAGGTTGAGGAATGGAACGAGTACTTCAAGA 132
QY 108 AGCCAGAGGAGGCGGCAAGCTGGTGTCTGACTTCTGCGCCCTGTCAGTGGGT 167
Db AGCGCTTGGAGACTTAAGAACTGTGTGTGTCGATTTTCTGCTTCATGTGCGGSCCT 192
QY 168 GCCAGATGATGGCCCGGTGTACCGGACTCGCCAGCAAGTACCTTCGCGGTCTTCC 227
Db GCCGTTTATTGCCCCAATTCCTTGTGACATTCCTAAGAGATGCCCATGTTATATTC 252
QY 228 TCGAGGTGCGAGCTGCGAGACTGCTGGAAGTCGCG-CAAGATCTACGCGCTCATGTG 286
Db TCAAGTTGATGTTGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 312
QY 287 CCGACCTTCTGCTTCATCAGGAACGCGGAGACGCTCGAGAGCTTTTGTACCGTCGACG 346
Db CCAACTTTTCTTCTTATTAAGATGAAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 372
QY 347 GAGCGCTCCGGGACCGCTCAGAGAGTACCGCGCTCGAGAGCTTTTGTACCGTCGACG 406
Db GAGGAGTTGCGAGCAGACCATGATGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 432
QY 407 TC 408
Db 433 TC 434
RESULT 9
US-08-444-803-103
Sequence 103, Application US/08444803
Patent No. 565414
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christopher
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Utnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC

Tue May 11 16:02:01 2004

;; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
;; NUMBER OF SEQUENCES: 106
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: CIBA-GEIGY Corporation
;; STREET: 7 Skyline Drive
;; CITY: Hawthorne
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10532
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/444,803
;; FILING DATE: 19-MAY-1995
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/181,271
;; FILING DATE: 13-JAN-94
;; APPLICATION NUMBER: US 08/093,301
;; FILING DATE: 16-JUL-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/937,197
;; FILING DATE: 6-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/678,378
;; FILING DATE: 1-APR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/305,566
;; FILING DATE: 6-FEB-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/165,667
;; FILING DATE: 8-MAR-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/042,847
;; FILING DATE: 6-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/632,441
;; FILING DATE: 21-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/425,504
;; FILING DATE: 20-OCT-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/848,506
;; FILING DATE: 6-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/768,122
;; FILING DATE: 27-SEP-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/580,431
;; FILING DATE: 7-SEP-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/368,672
;; FILING DATE: 20-JUN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/329,018
;; FILING DATE: 24-MAR-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/045,957
;; FILING DATE: 12-APR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elmer, James Scott
;; REGISTRATION NUMBER: 36,129
;; REFERENCE/DOCKET NUMBER: S-19825/P1/COC 1727
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)541-8614
;; TELEFAX: (919)541-8689
;; INFORMATION FOR SEQ ID NO: 103:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 653 base pairs
;; TYPE: nucleic acid

;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-444-803-103
Query Match 12.5%; Score 87.6; DB 1; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-09;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;
QY 48 CCGAGGAGGGTCCGCGTATCGGTGCCACACCAAGGACGAGTTCGACCCCGCATGGCCA 107
DB 73 CCGAGGAGGGACAGTGTTCGCTGCCACCAAGGTTGAGGAATGGAACGAGTACTTCAAGA 132
QY 108 AGGCCAAGGAGCAGGGCAAGCTGTGTCATCGATTCATGCCCCCTGGTGCAGTGGT 167
DB 133 AAGGCGTTGAGACTAAGAAACTGGTGGTGGTATTTACTGCTTCATGGTCCGSCCTT 192
QY 168 GCCAGATGATGCCCGGCTGTACGGGACTGGCCAGCAGTACCTTCCGCGGTCTTCC 227
DB 193 GCGGTTTATTGCCCAATTTCTTGATCTCTTCTTGAAGATGCTTATATATATATCC 252
QY 228 TCGAGTTCGACGTTCGACCAACTGCTTGGAAAGTCCGCGCTTCCGCGGTCTTCC 286
DB 253 TCAGGTTGATGTTGATGAATCTGAAGACTGTTTCAGCGGAATGGAAGTGTGGAGGCAATG 312
QY 287 CCGACCTTCTGCTTCATCAGGACCGGAGACGCTCGAGAGCTTTGCTACCGTCCGACGAG 346
DB 313 CCAACTTTTGTCTTCAATAAGATGGAAGAAAGAGTGGACAGAGTGTGGTCCAGAGAA 372
QY 347 GACGAGCTCCGGAGCGCCCTCAGGAAGTACGGCGCGCTGGGCACTACGACGGCTCCTGCC 406
DB 373 GAGGAGTTCAGCAGACCATAGTGAAGCATGCTGCTCCTGCTACTGTCTACTGCTTCAATC 432
QY 407 TC 408
DB 433 TC 434
RESULT 10
US-08-449-043-103
; Sequence 103, Application US/08449043
; Patent No. 5689044
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.
; APPLICANT: Goodman, Robert M.
; APPLICANT: Harms, Christian
; APPLICANT: Meins, Jr., Frederick
; APPLICANT: Montoya, Alice
; APPLICANT: Moyer, Mary B.
; APPLICANT: Neuhaus, Jean-Marc
; APPLICANT: Payne, George B.
; APPLICANT: Sperison, Christoph
; APPLICANT: Stinson, Jeffrey R.
; APPLICANT: Uknes, Scott J.
; APPLICANT: Ward, Eric R.
; APPLICANT: Williams, Shericca C.
; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,043
 FILING DATE: 24-MAY-1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/181,271
 FILING DATE: 13-JAN-94
 APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/042,847
 FILING DATE: 6-APR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/632,441
 FILING DATE: 21-DEC-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/425,504
 FILING DATE: 20-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/848,506
 FILING DATE: 6-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/768,122
 FILING DATE: 27-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/580,431
 FILING DATE: 7-SEP-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/368,672
 FILING DATE: 20-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/329,018
 FILING DATE: 24-MAR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/045,957
 FILING DATE: 12-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8614
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 103:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 653 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-449-043-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;
 Best local Similarity 54.4%; Pred. No. 2.7e-09;
 Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;
 Qy 48 CCGAGGAGGCGCGTGCATCGCGTGCACACCAAGGAGGTTCCAGCGCCCGCATGGCCA 107
 Db 73 CCGAGGAGGAGGAGGAGGTTCCAGCGCGCGTGCATCGCGTGCACACCAAGGAGGTTCCAGG 132

Qy 108 AGGCAAGAGGAGGCGCAAGCTGGTGTCTCATGCACTTCATGCGCCCTCGTGTGAGTGGGT 167
 Db 133 AAGCGGTGAGACTAAGAACTGGTGTGGTGGATTTTACTGCTTCATGTTGGGSCCTT 192
 Qy 168 GCCAGATGATGGCCCGGTGTACGCGGACTGCGCAAGTACCTTCCCGGTCCTCC 227
 Db 193 GCGCTTTATTTGCCCCAATCTTCTGCTGACATTTGTAAGAGATGCCCATGTTATATCC 252
 Qy 228 TCGAGGTGAGCTGCGACGAACCTCTGGAAGTCGG- GAAGATCTACGGCGTCCATGTGATG 286
 Db 253 TCAAGGTTGATGTTGATGAACCTGAAGACTCTTTTTCAGCGGGAATGGAGTGTGGAGCAATG 312
 Qy 287 CCGACCTTCTGCTTCATCAGACGCGGAGACGCTCGAGAGCTTTGCTACCGTCGAGAG 346
 Db 313 CCAACTTTCTTCATTAAAGATGGAAGAGAAAGTGCACAGAGTTGTTGGTGCCAGAAA 372
 Qy 347 GACGAGCTCGGAGCGGCTGCAAGAGTACGCGCGCTGCGACTAGCAGCGCTCTCGCC 406
 Db 373 GAGGAGTTGCAGCAGACCATAGTGAAGCATGCTGCTCTCTACTGTCTGCTTGAATC 432
 Qy 407 TC 408
 Db 433 TC 434

RESULT 11

US-08-456-265A-103
 ; Sequence 103, Application US/08456265A
 ; Patent No. 5767369

GENERAL INFORMATION:

APPLICANT: Alexander, Danny C.
 APPLICANT: Ryals, John A.
 APPLICANT: Goodman, Robert M.
 APPLICANT: Stinson, Jeffrey R.
 TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
 TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
 NUMBER OF SEQUENCES: 111
 CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,265A
 FILING DATE: 31-MAY-95

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/181,271
 FILING DATE: 13-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/093,301
 FILING DATE: 16-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197
 FILING DATE: 6-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/678,378
 FILING DATE: 1-APR-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/305,566
 FILING DATE: 6-FEB-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/165,667
 FILING DATE: 8-MAR-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-456-265A-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-05;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

Qy 48 CCGAGGAGGTCGCGTATCGCGTCCACACCAAGGACGAGTTGGAGCGCGCATGCCCA 107
Db 73 CCGAGGAGGTCGCGTATCGCGTCCACACCAAGGTTGAGGAATGGAAACGAGTACTTCAAGA 132
Qy 108 AGCCAGGAGGACGGGCAAGCTGTGTCTCATGCGCCCTCGTGCAGTGGGT 167
Db 133 AAGCGTTGAGACTAAGAACTGTGTGTGTCTGATTTTCTGTTCTATGTTGCGGSCCTT 192
Qy 168 GCCAGATGATGCGCCCGGTGTACCGGAGTGCAGCAAGTACCCCTTCCCGGTCTTCC 227
Db 193 GCGGTTTATTTGCCCAATCTTCTGCTGACATTTCTAAGAAATGCCCAATGTTATATTTCC 252
Qy 228 TCGAGGTGCGCTCGAGCAAGCTGTGAGTCCG-AGAGTCTACGCGTCCATGTCATG 286
Db 253 TCAAGGTTGATGTTGATGAATGAACTGTTTCAGCGGATGAGTGTGGAGCAATG 312
Qy 287 CCGACCTTCTGCTTCTATCAGGAACGGCGAGACGCTCGAGAGCTTTTGTTCGTCGAGAG 346
Db 313 CCACTTTTGTCTTCAITTAAGATGAAAGAGTGGACAGAGTGTGTTGTCGCAAGAA 372
Qy 347 GACAGCTCCGGAGCGCGTCAAGAGTACCGCGCTGGCACTACGAGGCTCTGCC 406
Db 373 GAGGAGTTGCAGCAGACCATATGAGCAGTCTGCTCTGCTACTGTCACCTGCTGATC 432
Qy 407 TC 408
Db 433 TC 434

RESULT 12
US-08-455-416-103
Sequence 103: Application US/08455416
Patent No. 5777200
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uxnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10512
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA: US 07/937,197
APPLICATION NUMBER:
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:

RESULT 13
US-08-455-244-103
; Sequence 103, Application US/08455244
; Patent No. 5789214
; GENERAL INFORMATION:
; APPLICANT: Ryals, John A.
; APPLICANT: Alexander, Danny C.
; APPLICANT: Beck, James J.
; APPLICANT: Duesing, John H.
; APPLICANT: Friedrich, Leslie B.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/454,876
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-244-103

APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-455-244-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-09;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;
QY 48 CCGAGGAGGTCGCGTGTGATCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCATGGCCA 107
DB 73 CCGAGGAGGACAAAGTGTGGCTGCGCACACAGGTTGAGGAATGGAACGAGTACTTCAAGA 132
QY 108 AGCCCAAGGAGCGGCAAGCTGGTGCATCGACTTCATGCCCCCTCGTGCAGTGGGT 167
DB 133 AAGCGGTGAGACTAAGAAACTGGTGGTGCATTTTACTGCTTCAATGTCGGSCCTT 192
QY 168 GCCAGATGATGGCCCGGTGTACGCGACTGCGCCAGCAAGTACCTTCGCGGCTCTCC 227
DB 193 GCGTTTATGCCCCCAATCTTCTGACATTCTAAGAGATGCCCATGTATATTC 252
QY 228 TCGAGTTCGACGTGCGACAACTCTGGAAGTGC-GAAGATCTACGCGGTCCATGTGATG 286
DB 253 TCAAGGTGATGTGATGAACTGAAGTCTTTTCAGCGGAATGGAATGTTGGAGGCAATG 312
QY 287 CCGACCTTCGCTTCATCAGGACGCGGAGAGCTGAGAGCTTGTCTACCGTCGACGAG 346
DB 313 CCAACCTTCTCTTCATTAAGATGGAAGAGAGTGGACAGATTTGTTGGTCCAGAA 372
QY 347 GACGAGTCCGGAAGCGCGTCAGGAAGTACGCGCGCTGGCATAGACGGCTCTCTGCC 406
DB 373 GAGGAGTTGACGAGACCAATAGTGAAGCATGCTCTCTCTACTGTCACTGCTTGAATC 432
QY 407 TC 408
DB 433 TC 434

RESULT 14
US-08-454-876-103
Sequence 103, Application US/08454876
Patent No. 5804693
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John W.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.


```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-454-876-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-09;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

Qy 48 CCGAGGAGGGTGCCTGATCGCGTCCACCAAGGACGAGTTCGACGCCGCGATGGCCA 107
Db 73 CCGAGGAGGGCAAGTGTTCGGCTGCCACAGGTTGAGAAATGCAACGAGTACTTCAAGA 132
Qy 108 AGCCCAAGCAGCAGGCGAGTGTGTCATCGACTTCATGCCCTTGGTGGCAGTGGT 167
Db 133 AAGCGTTGAGACTAAGAACTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 192
Qy 168 GCCAGATGATGCCCGCGGTGTACCGGAGTCCGCGCAGCAAGTACCTTCCCGGTCTTCC 227
Db 193 GCGCTTTATTTGCCCAATCTTCTGACATTGCTAAGAGATGCCCATGTTATATTC 252
Qy 228 TCGAGGTGCGCTGACCACTCTGGAAGTCCG- GAAGATCTAGGCGTCCATGTGATG 286
Db 253 TCAAGGTTGATGTTGATGAACCTGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGCAATG 312
Qy 287 CCGACTTCTCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTACCGTTCGACGAG 346
Db 313 CCACTTTGCTTCATTAAGATGGAAGAGAGTGGACAGATGTTGGTGCCAAGAA 372
Qy 347 GACGAGTCCCGGAGCGCTGAGGAAGTACGCGCGCGTGGCACTACGACGGCTCTTCC 406
Db 373 GAGGAGTTGCAGCAGACCATAGTAGTGAAGCATGCTGCTCTGCTACTGTCTGCTGATC 432
Qy 407 TC 408
Db 433 TC 434

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RESULT 15

US-08-457-364-103
Sequence 103, Application US/08457364
Patent No. 5847258

GENERAL INFORMATION:

APPLICANT: Ryals, John A.
APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
APPLICANT: Duesing, John H.
APPLICANT: Friedrich, Leslie B.
APPLICANT: Goodman, Robert M.
APPLICANT: Harms, Christian
APPLICANT: Meins, Jr., Frederick
APPLICANT: Montoya, Alice
APPLICANT: Moyer, Mary B.
APPLICANT: Neuhaus, Jean-Marc
APPLICANT: Payne, George B.
APPLICANT: Sperison, Christoph
APPLICANT: Stinson, Jeffrey R.
APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 653 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-364-103

Query Match 12.5%; Score 87.6; DB 2; Length 653;
Best Local Similarity 54.4%; Pred. No. 2.7e-09;
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

Qy 48 CCGAGGAGGGTGCCTGATCGCGTCCACCAAGGACGAGTTCGACGCCGCGATGGCCA 107

73	CGAGGAGCGGACAGTGTTCGGCTGCCACAAAGGTTGGGNAATCGAACGAGTACTTCCAAGA	133
108	AGGCCAAGGAGCAGGGCGAAGCTGGTGGTGCATCGACTTCATGGCCCCCTGGTCGASTGGGT	167
133	AAGCGGTTGAGACTAAGAAAACCTGGTGGTGGTGCATTTTACTGCTTCATGGTCCGGSCCTT	192
168	GCCAGATGATGGCCCCCGGTGTACCGGACATGGCCAGCAAGTACCTTCCCGCGGTCTTCC	221
193	GCCGTTTATTTGCCCAATCTTGGCTGACATTCGTAAGAAGATGCCCAATGTATATATCC	252
228	TCGAGGTCGACGTCGACGAACCTGCTGGAGTCCGCG - GAAATCTACCGGCTCCATGTGATG	286
253	TCAAAGTTTGATGTTTGATGAACATGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGGCAATG	312
287	CGACCTTTCTCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTTGTCTACGCTCGACGAG	346
313	CCAACTTTTGTCTTCATTAAAGATGGAAAAGAGTGACACAGAGTTGTTGGTCCCAAGAAA	372
347	GACGAGCTCCGGGACGGCTCAGAGGATGACCGCGCTGGCACTACGACGGCTCCTGCC	406
373	GAGGAGTTGCGAGCAGACCAATGATGAAGCATGCTGCTCTGCTACTGTCTACTGCTGCTGAATC	432
407	TC	408
433	TC	434

Search completed: May 5, 2004, 23:29:36
Job time : 60.7917 secs

1	613	87.6	731	13	US-10-425-114-16798	Sequence 16738, A
2	613	87.6	742	13	US-10-425-114-16904	Sequence 16904, A
3	613	87.6	752	13	US-10-425-114-17028	Sequence 17028, A
4	492.4	70.3	780	13	US-10-425-114-7100	Sequence 7100, App
5	379.4	54.2	647	13	US-10-425-114-18407	Sequence 18407, A
6	208.8	29.8	737	13	US-10-425-114-35090	Sequence 35090, A
7	207.2	29.6	548	13	US-10-425-114-23500	Sequence 23500, A
8	207.2	29.6	588	13	US-10-425-114-23471	Sequence 23471, A
9	207.2	29.6	591	13	US-10-425-114-23498	Sequence 23498, A
10	205.6	29.4	565	13	US-10-425-114-35628	Sequence 35628, A
11	205.6	29.4	577	13	US-10-425-114-6528	Sequence 6528, App
12	205.6	29.4	583	13	US-10-425-114-284	Sequence 284, App
13	205.6	29.4	594	13	US-10-425-114-17618	Sequence 17618, A
14	205.6	29.4	692	13	US-10-425-114-23337	Sequence 23337, A

76	CGTGTATCGCGTGCCACACAAGAGCAGAGTTCGAGCGCCGCGATGCGCAAGGCCAAGGAGCA	135
121	GGCGAAGCTGGTGGTGCATCGACTTCATCGCCGCCCTGGGTGCGAGTGGGTGCCAGATGATGGC	180
136	GGCGAAGCTGGTGGTGCATCGACTTCATCGCCGCCCTGGGTGCGAGTGGGTGCCAGATGATGGC	195
181	CCCGGGTGTACCGGAGTCCGCGACGACAGTACGCTTCGCGGGTCTTCTCGAGGTCCGACGT	240
196	CCCGGTGTACCGGAGTCCGCGACGACAGTACCTTCGCGGGTCTTCTCGAGGTCCGACGT	255
241	CGACGAACTGCTGGAAGTTCGCGAAGATCTACGGGGTGCATGTGCATGCCGACCTTCTGCTT	300
256	CGACGAACTGCTGGAAGTTCGCGAAGATCTACGGGGTCCATGTGTATGCCGACCTTCTGCTT	315
301	CATCAGGAACCGCGAGAGCGCTCGAGAGCTTGTCTACCGTCGACGAGAGCAGAGTCCGGGA	360
316	CATCAGGAACCGCGAGAGCGCTCGAGAGCTTGTCTACCGTCGACGAGAGCAGAGTCCGGGA	375
361	CGCGCTCAGGAAGTACGCGCGCGCTGGGCATCTACGACGGCTCCCTGCTCGCGCTCCGCTTA	420
376	CGCGCTCAGGAAGTACGCGCGCGCTGGGCATCTACGACGGCTCCCTGCTCGCGCTCCGCTTA	435
421	ATTCAGGAGATGTGATGGTGTAGCAAAATAGCGCGCGCGACCGAGTCGTCAATAAATA	480
436	ATTCAGGAGATGTGATGGTGTAGCAAAATAGCGCGCGCGACCGAGTCGTCAATAAATA	495
481	AATAAATAAATAAATAAATAAATAAATAAAGGCCAACGTCACGACGCAAAATTAGTG	540
488	AATAAATAAATAAATAAATAAATAAATAAAGGCCAACGTCACGACGCAAAATTAGTG	547
541	CGCGCGCGGTAGTACTGACAGAGTATCGCGCACTGCTGTGATGTCAGTTGGTC	600
548	CGCGCGCGGTAGTACTGACAGAGTATCGCGCACTGCTGTGATGTCAGTTGGTC	607
601	GTTTAAAGTGATGTAGTGTGTACTATGTTTCAGTCCGA	639
608	GTTTAAAGTGATGTAGTGTGTACTATGTTTCAGTCCGA	646

RESTIT. 4

```

US-10-425-114-7100
; Sequence 7100, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7100
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700617241_FLI
US-10-425-114-7100

```

Query Match	70.3%	Score	492.4;	DB	13;	Length	780;
Best Local Similarity	92.4%;	Prod. NO.	1.9e-99;				
Matches	606;	Conservative	0;	Mismatches	16;	Indels	34;
						Gaps	7;

1	GGATCCACACCCGAGG-----AAAGAGAGAGGAGGTCGGAATTAATCGCGCCGAGAG	55
57	GGATCCACACCCGAGGAAATTAAGAGAGAGAGAGGTCGGAATTAATCGCGCCGAGAG	116
56	GGTCCCGGTGATCGCGTCCACACCAAGGACGAGTTCGAGCCCGCATGCGCCAAGCCCAAG	115

117	Db		GGTGGGTTGATCGGTGCGCACCAAGGACGAGTTTCAGCGCCCGCATGGCCAAAGGCGCAAG	176
116	QY		GAGCAGGCGAAGCTGGTGGTTCATCGACTTCATGCGCCCGCTGGTGCGAGTGGGTGCGAGATG	175
177	Db		GAGGAGGGCGAAGCTGGTGGTTCATCGACTTCATGCGCCCGCTGGTGCGAGTGGGTGCGAGATG	236
176	QY		ATGCGCCCGGTTGATCGCGGACTGGCGCCAGCAAGTACCGCTTCCGCGGCTCTTCCTCGAGGTC	235
237	Db		ATGCGCCCGGTTGATCGCGGACTGGCGCCAGCAAGTACCGCTTCCGCGGCTCTTCCTCGAGGTC	296
236	QY		GAGGTGCGACGAACCTGCTGGAGTTCGGAAAGANTCTA GCGGTCATGTGATGCGACCTTC	295
297	Db		GAGCTCGACGAACCTGCTGGAAAGTTCGGAAAGANTCTA GCGGTCATGTGATGCGACCTTC	356
296	QY		TGCTTCATCAGGAACGCGGAGACGCTCCAGAGCTTTTGCTACCGTCGACGAGGACGAGCTC	355
357	Db		TGCTTCATCAGGAACGCGGAGACGCTCCAGAGCTTTTGCTACCGTCGACGAGGACGAGCTC	416
356	QY		CGGGACGCGTCCGGAAGTA-----CGCGCGCGCTGGCGACTACGAGCGGCTCTGCTCG	409
417	Db		CGGAAAGCGCGTCAGGAAGTACGCGCGCGCGCGCGCGCGGCGGCGACTACGAGCGGCTCTGCTCG	476
410	QY		GCGTCCGCGCTAATTC--AGGAGAGTCACTGTGTAGCAAAATAGCGCGCGCGG--CACAGTCG	466
477	Db		GAGTCCGCGCTAATCCAGNAGACCTGATCATGTGTAGCAAAACAGCGCGCGGCTCACCAGTCG	536
467	QY		TCATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGGCCAAACGTACG	526
537	Db		TCATAAATAA-----TAAATAAATAAATAAATAAATAAATAAATAAAGGCCAAACTTACG	581
527	QY		ACGACAAATATAGTGGCGCGCGTACTAGCTAGCAGAGTATGCGCGCGC---ACTGTGT	583
582	Db		ACGACAAATATAGTACGCGCGCGGTAGCTAGCAGAGATATGCGCGCGGCACTACTGTGT	641
584	QY		CGATCTGCAGTTTGGTGGTTTAAAGTGATTGTAGTGTGTACTATGTTTCAGCTCGA	639
642	Db		CGATCTGCAGTTTGGTGGTT--CAAGTGAATTGATTGTACTATGTTTCAGCTCGA	695

RESULTS

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US-10-425-114-19407
; Sequence 19407, Application US/10425114
; Publication NO. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19407
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3079-042-C1_FLI
US-10-425-114-19407

```

Query Match	54.2%	Score 379.4	DB 13	Length 647
Best Local Similarity	95.5%	Pred. NO. 2.1e-74		
Matches 404	Conservative 0	Mismatches 11	Indels 8	Gaps 1
QY	217	CGCGGTCTTCCTCAGCTCGCACTCGACGAACTGTGGAGTCCGCGAAGCTACCGGCT	276	
Dd	148	CGCGCGGCAGCGCGGCATCGACTGGAACACTGCTCGAACTCGCGAAGCTACCGGCT	207	

Qy	277	CCATGTGATGCGACGCTTCTGCTTCATCAGAAACGGCGAGACGCTCGAGAGCTTTGCTTAC	336
Db	208	CCATGTGATGCGGACGCTTCTGCTTCATCAGAAACGGCGAGACGCTCGAGAGCTTTGCTTAC	267
Qy	337	CGTCGACGAGGACGAGCTCGGGACGCGCTCAGAGACTACGCCGCGCTGGGCACTACGAC	396
Db	268	CGTCGACGAGGACGAGCTCGGGACGCGCTCAGAGACTACGCCGCGCTGGGCACTACGAC	327
Qy	397	GGCTCTCGCTCGGCGTCCGCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGGC	456
Db	328	GGCTCTCGCTCGGCGTCCGCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGGC	387
Qy	457	GCACAGCTGCTCAATTAATAATAATAATAATAATAATAATAATAATAATAATAAAGG	516
Db	388	GCACAGCTGCTC-----AATAATAATAATAATAATAATAATAATAATAATAAAGG	439
Qy	517	CCAACTAGCAGCAAAATTAGTCGGCGCGCGGTACTAGCAGAGATGATGCGCGCGC	576
Db	440	CCAACTAGCAGCAAAATTAGTCGGCGCGCGGTACTAGCAGAGATGATGCGCGCGCC	499
Qy	577	ACTGTGTCGATCTGCAGTTTGGTCGTTTAAAGTGAATTGTAGTGTGTACTGTATTCAGCT	636
Db	500	ACTGTGTCGATCTGCAGTTTGGTCGTTTAAAGTGAATTGTAGTGTGTACTGTATTCAGCT	559
Qy	637	CGA 639	
Db	560	CGA 562	

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RESULT 6
US-10-425-114-35090
? Sequence 35090, Application US/10425114
? Publication No. US20040034888A1
? GENERAL INFORMATION:
? APPLICANT: Liu, Jingdong
? APPLICANT: Zhou, Yihua
? APPLICANT: Kovalic, David K.
? APPLICANT: Screen, Steven E
? APPLICANT: Tabaska, Jack E
? APPLICANT: Cao, Yongwei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-21(53313)B
? CURRENT APPLICATION NUMBER: US/10/425,114
? CURRENT FILING DATE: 2003-04-28
? NUMBER OF SEQ ID NOS: 73128
? SEQ ID NO 35090
? LENGTH: 737
? TYPE: DNA
? ORGANISM: Zea mays subsp. mexicana
? FEATURE:
? OTHER INFORMATION: Clone ID: UC-ZMFLTBOSINTE079E9_FLI
US-10-425-114-35090

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	Query Match	29.8%;	Score 208.8;	DB 13;	Length 737;
	Best Local Similarity	72.6%;	Prod. No. 1.5e-36;		
	Matches 270;	Conservative 0;	Mismatches 102;	Indels 0;	Gaps 0;
Qy	36	GAATATGGCGCGCAGAGGGTCCGTGATCGCGTGCCACACCAAGACAGATCGACG	95		
Db	86	GATCAATGGCTCCGAGCAGGGATCGTGATCGCGTGCCACAAAGGCTGGATTCGACG	145		
Qy	96	CCCGCATGGCCCAAGGCCAAGACGAGCGCAAGCTGGTGGTCACTGACTTCATGGCCCGCT	155		
Db	146	CCCAATGACCAAGGCCCAAGAACCGGCAAGCTGGTGGTCACTGACTTCATCGCGGCT	205		
Qy	156	GGTCAGTGGGTGCCAGATGATGGCCCGCGGTGTACGGCGACTGGCCAGCAAGTACCGTT	215		
Db	206	GGTGGGTCCTTCCATGGCCGGCGCCATCGCCCCACTGTTCTGTCGAACAACCCAGGAAGTTCATC	265		
Qy	216	CCGCGGTCTTCCTTCAGGTGCACCGTCGACGAACTGCTCGAAAGTCGCGAAGTCTACCGCGC	275		
Db	266	AGGTGCTCTCTCTGAAGTGTGAGGTGGACGAAAGTGAACCAAGTCAACCGCGCTTACGAGG	325		

Qy	276	TCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGTCTA	335
Db	326	TCGAGGCGATGCCGACCTTCCACTTCTCAAGAACGGCAAGCGTTCGCGACCATCGTGG	385
Qy	336	CCGTGAGCAGGACGAGCTCGGGAACGCCGTGAGGAAGTACGCCCGCGCTGGCACTACGA	395
Db	386	GTGCCAAGAGGACGAGCTCTGCGCCCTGATCGAGAAGCATGCCCGCGCTGCGCTGCCT	445
Qy	396	CGGCTCCTGCCT	407
Db	446	CTGCGTCTGCCT	457

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RESULT 7
US-10-425-114-23500
; Sequence 23500, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23500
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-057-G4_FLI
US-10-425-114-23500

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Query Match	29.6%; Score 207.2; DB 13; Length 548;
Best Local Similarity	72.3%; Pred. No. 3e-36;
Matches 269; Conservative	0; Mismatches 103; Indels 0; Gaps 0;
Qy	36 GAATAATGGCGGCGGAGGAGGGTCCGTGATCGCTGCCACACCAAGACGAGTTCCGACG 95
Db	
Qy	55 GATCAATGGGTCCGACAGGGAGTCTGTATCCGTGCCACAGCAGGCTGAGTTCCGACG 114
Db	
Qy	96 CCGCATGGCCAAAGGCCAGGAGCAGGGCAAGCTGGTGTTCATCGACTTCATGGCCCCCT 155
Db	
Qy	115 CCCACATGACCAAGGCCAGGAAGCGGCAAGCTGGTGTTCATCGACTTCACCTGCCGCT 174
Db	
Qy	156 GTTGCAATGGTCCAGATGATCGGCCCGGGTACCGGAGTCTGCCGACGCAAGTACCCCT 215
Db	
Qy	175 GGTGGGTCATCGCCGGCCATCGCCCACTGTTCTGCGAACACGCCAAGAGTTTCACT 234
Db	
Qy	216 CCGGGTCTTCCTCGAGTGCAGCTCGACAACTGCTGGAAGTCGCGAAGATCTACGGCG 275
Db	
Qy	235 AGTTCGTTCTCTGAAGTGCAGTGCAGCAAGTGAAGGAAGTCAACGGCGCCTACGAGG 294
Db	
Qy	276 TCAATGTGATGCCGACCTTCTGCTTCATCAGGAACCGCGAGAGCGCTCGAGAGCTTTGCTA 335
Db	
Qy	295 TCGAGGCGATGCCGACCTTCACCTTCGTCAAGAACCGCAAGCGGTGCGACCATCGTGG 354
Db	
Qy	336 CCGTTCACGAGGACGAGCTCCGGGACCGCCTCAGGAAGTACGGCCCGCGCTGGCAGCTACGA 395
Db	
Qy	355 GTGCCAAGAGACGAGCTCTGGCCCTGTATCGAAGAGCATGCCGGCCCTCGCGCTCGCT 414
Db	
Qy	396 CGGCTCTGCT 407
Db	
Qy	415 CTGGCTGCTGCT 426
Db	

RESULT 8

[illegible]

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US-10-425-114-23471
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23498
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3596-057-A2_FLI
US-10-425-114-23498

Query Match      29.6%; Score 207.2; DB 13; Length 591;
Best Local Similarity 72.3%; Pred. No. 3.le-36;
Matches 269; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCAGGAGGGTGCCTGATCCGTGTCACCAAGGACGAGTTGCGAG 95
DB 51 GATCAATGCGCTCCGAGCACGGAGTGCTGATCCGTGCCACGAAGGCTGAGTTGCGAG 110
QY 96 CCGCATGCGCGAAGGCGCAGGACGAGCGCAAGCTGTGTGTCATCGACTTTCATGCGCCCCCT 155
DB 111 CCACATGACCAAGGCCCGGAAAGCCGCGCAAGCTGTGTGTCATCGACTTTCATGCGCCCCCT 170
QY 156 GGTCAGTGGGTGCCAGATGATGCGCCCCCGGTGTACCGGAGTTCGCGCAGCAAGTACCTT 215
DB 171 GTGCGGTCCATGCGCGCCATCGCCCCTGTTCGTGCAACACGCGCAAGAGTTCACTC 230
QY 216 CCGCGTCTTCCTCGAGTTCGAGTTCGAGCAAGCTGTGTGTCATCGACTTTCATGCGCCCCCT 275
DB 231 AGTGTGCTCTTCCTGAGGTGCGAGTTCGAGCAAGCTGTGTGTCATCGACTTTCATGCGCCCCCT 290
QY 276 TCCATGTGATGCGCGACCTTCTGTTCATCGAGAACCGCGAGACGCTCGAGAGCTTTGCTA 335
DB 291 TCAGGCGATGCGCGACCTTCCACTTTCGTCAAGAAGCGCAAGAGCGTTCGCGACCATCTGG 350
QY 396 CGGCTCTCTGCT 407
DB 411 CTGCGTCTGCT 422

RESULT 10
US-10-425-114-35628
; Sequence 35628, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCES: Plants and Uses Thereof for Plant Improvement
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35628
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROB73071D12_FLI
US-10-425-114-35628

Query Match      29.4%; Score 205.6; DB 13; Length 565;
Best Local Similarity 72.0%; Pred. No. 5.8e-36;
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCAGGAGGGTGCCTGATCCGTGTCACCAAGGACGAGTTGCGAG 95
```


Db 30 GATCAATGGCGTCCGAGCAGGAGTCTGTATCGTCCGTCACAGCAAGGCTGAGTTTCGAGC 89
Qy 96 CCCGCGATGGCCAGAGCCAGAGCAGGCGAGCTGTGTCTATCGACTTCATGGCGCCCT 155
Db 90 CCACATGACCAAGGCCAGAGAGCCGAGCTGTGTCTATCGACTTCATGGCGCCCT 149
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGGTGTACCGGACTCGCCCAAGTACCCCTT 215
Db 150 GGTGCGGTCCATGCGCGCCATCGCCCACTGTCTGTCGAACACGCCAAGAGTTCACTC 209
Qy 216 CCGCGGTCTCTTCGAGGTGCGAGTCTGCTGAGTCTGCGAGTCTGCGAGTCTACGCG 275
Db 210 AGTGTCTCTCTGAGAGGTGCGAGTCTGCTGAGTCTGCGAGTCTACGCG 269
Qy 276 TCCATGTGATGCGCACTTCTGCTCATCAGGAACGCGAGACGCTTCGAGACTTTGCTA 335
Db 270 TCGAGGCGATCGCCGACTTCCACTTCTGTCAGAACGCGCAAGCGGTGCGACCATCGTGG 329
Qy 336 CCGTCGACGAGGACGAGCTCCGCGAGCCGCTCAGGAAGTACGCGCCGCTGCCACTACGA 395
Db 330 GTGCCAGGAGGACGAGCTCTGCGCCCATCGAGATCGAGAGCATCGCGCGCTGCGCTGGT 389
Qy 396 CGGCTCTGCT 407
Db 390 CTGCTCTGCT 401

RESULT 11
US-10-425-114-6528
; Sequence 6528, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 6528
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700570172_FLI
US-10-425-114-6528

Query Match 29.4%; Score 205.6; DB 13; Length 577;
Best Local Similarity 72.0%; Pred. No. 6.9e-36;
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 36 GAATATGCGCGCCGAGGAGGTGCGTGTATCGGTGCGACACCAAGGAGGTTTCAGC 95
Db 40 GATCAATGCGTCCGAGCAGGAGTCTGTATCGGTGCGACAGCAAGGCTGAGTTTCAGC 99
Qy 96 CCGCATGCGCCAGGCCAAGAGCAGGCGAAGCTGTGTCTATCGACTTCATGGCGCCCT 155
Db 100 CCCATGACCAAGGCCAGGAGCGCGAAGCTGTGTGTCTATCGACTTCATCGCGCCCT 159
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGGTGTACCGGACTCGCCCAAGTACCCCTT 215
Db 160 GGTGCGGTCTCTGAGAGGTGCGAGTCTGCTGAGTCTGCGAGTCTACGCG 219
Qy 216 CCGCGGTCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 275
Db 220 AGGTGCTCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 279
Qy 276 TCCATGTGATGCGCACTTCTGCTCATCAGGAACGCGAGACGCTTCGAGAGCATCGCGCGCTTTCGCTA 335

Db 30 GATCAATGGCGTCCGAGCAGGAGTCTGTATCGTCCGTCACAGCAAGGCTGAGTTTCGAGC 339
Qy 336 CCGTCGACGAGGACGAGCTCCGCGAGCCGCTCAGGAAGTACGCGCGCTGCGACTACGA 395
Db 340 GTGCCAGGAGGACGAGCTCTGCGCCCATCGAGATCGAGAGCATCGCGCGCTGCGCTGCGA 399
Qy 396 CGGCTCTGCT 407
Db 400 CTGCTCTGCT 411

RESULT 12
US-10-425-114-284
; Sequence 284, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 284
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700052149_FLI
US-10-425-114-284

Query Match 29.4%; Score 205.6; DB 13; Length 583;
Best Local Similarity 72.0%; Pred. No. 6.9e-36;
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 36 GAATATGCGCGCCGAGGAGGTGCGTGTATCGGTGCGACACCAAGGAGGTTTCAGC 95
Db 42 GATCAATGCGTCCGAGCAGGAGTCTGTATCGGTGCGACAGCAAGGCTGAGTTTCAGC 101
Qy 96 CCGCATGCGCCAAGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 155
Db 102 CCCATGACCAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 161
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGGTGTACCGGACTCGCCCAAGTACCCCTT 215
Db 162 GGTGCGGTCTCTGAGAGGTGCGAGTCTGCTGAGTCTGCGAGTCTACGCG 221
Qy 216 CCGCGGTCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 275
Db 222 AGGTGCTCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 281
Qy 276 TCCATGTGATGCGCACTTCTGCTCATCAGGAACGCGAGACGCTTCGAGAGCATCGCGCGCTTTCGCTA 335
Db 282 TGAGCGCATGCGCCAGCTTCTGCTCATCAGGAACGCGAGACGCTTCGAGAGCATCGCGCGCTTTCGCTA 341
Qy 336 CCGTCGACGAGGACGAGCTCCGCGAGCCGCTCAGGAAGTACGCGCGCTGCGACTACGA 395
Db 342 GTGCCAGGAGGACGAGCTCTGCGCCCATCGAGATCGAGAGCATCGCGCGCTGCGCTGCGT 401
Qy 396 CGGCTCTGCT 407
Db 402 CTGCTCTGCT 413

RESULT 13
US-10-425-114-17618
; Sequence 17618, Application US/10425114

Publication No. US20040034868A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 17618
LENGTH: 594
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3070-001-G9_FLI
US-10-425-114-17618

Query Match 29.4%; Score 205.6; DB 13; Length 594;
Best Local Similarity 72.0%; Pred. No. 6.9e-36;
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCGAGGAGGTCGCGTGCATCGCGTGCACACCAAGGACGAGTTGACG 95
Db 53 GATCAATGCGCGTCGAGCGAGGAGTGTGATCGGTGCCACAGCAAGCTGAGTTGACG 112
QY 96 CCGCATGCGCAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 155
Db 113 CCCACATGACCAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 172
QY 156 GTGTCAGTGGTGCACAGATGATGCGCGCGTGCATCGCGTGCACACCAAGGAGTACCCCTT 215
Db 173 GTGTCAGTGGTGCACAGATGATGCGCGCGTGCATCGCGTGCACACCAAGGAGTACCCCTT 232
QY 216 CCGCGGTCTTCTCGAGGTCGACGTCGACGTCGACGTCGACGTCGACGTCGACGTCG 275
Db 233 AGTGTGTCCTTCTGAGGTCGACGTCGACGTCGACGTCGACGTCGACGTCGACGTCG 292
QY 276 TCCATGTGATGCGGAGCTTCTGCTTCATCAGGAGCGGAGGAGGAGGAGGAGGAGG 335
Db 293 TGAGGCGATGCGGAGCTTCTGCTTCATCAGGAGCGGAGGAGGAGGAGGAGGAGG 352
QY 336 CCGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 395
Db 353 GTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 412
QY 396 CGGCTCTGCGCT 407
Db 413 CTGCGTCTGCGCT 424

RESULT 14
US-10-425-114-23337
Sequence 23337, Application US/10425114
Publication No. US20040034868A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 23337

LENGTH: 692
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3595-039-B9_FLI
US-10-425-114-23337

Query Match 29.4%; Score 205.6; DB 13; Length 692;
Best Local Similarity 72.0%; Pred. No. 7.4e-36;
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCGAGGAGGTCGCGTGCATCGCGTGCACACCAAGGAGGAGTTGACG 95
Db 11 GATCAATGCGCGTCGAGCGAGGAGTGTGATCGGTGCCACAGCAAGCTGAGTTGACG 70
QY 96 CCGCATGCGCAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 155
Db 71 CCCACATGACCAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 130
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QY 216 CCGCGGTCTTCTCGAGGTCGACGTCGACGTCGACGTCGACGTCGACGTCGACGTCG 275
Db 191 AGTGTGTCCTTCTGAGGTCGACGTCGACGTCGACGTCGACGTCGACGTCGACGTCG 250
QY 276 TCCATGTGATGCGGAGCTTCTGCTTCATCAGGAGCGGAGGAGGAGGAGGAGGAGG 335
Db 251 TCGAGGCGATGCCGAGCTTCCACTTGTGTCAGGAGCGGAGGAGGAGGAGGAGGAGG 310
QY 336 CCGTCGACGAGGAGGAGCTCCGCGGAGCGCGTCCAGGAGGAGGAGGAGGAGGAGGAGG 395
Db 311 GTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 370
QY 396 CGGCTCTGCGCT 407
Db 371 CTGCGTCTGCGCT 382

RESULT 15
US-10-260-238-5754
Sequence 5754, Application US/10260238
Publication No. US20040016025A1
GENERAL INFORMATION:
APPLICANT: Budworth, Paul R.
APPLICANT: Moughamer, Todd G.
APPLICANT: Briggs, Steven P.
APPLICANT: Cooper, Bret
APPLICANT: Glazebrook, Jane
APPLICANT: Goff, Stephen A.
APPLICANT: Katagiri, Fumiyaki
APPLICANT: Kreps, Joel
APPLICANT: Provart, Nicholas
APPLICANT: Rickes, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
CURRENT APPLICATION NUMBER: US/10/260,238
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/325,448
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 5754
LENGTH: 366
TYPE: DNA
ORGANISM: Zea mays
US-10-260-238-5754

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Query Match      29.0%; Score 202.8; DB 16; Length 366;
Best Local Similarity 72.1%; Pred. No. 2.4e-35;
Matches 264; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 41 ATGGCGCGCGAGGAGGCGGTGATCGCGTGCACACCAAGGACGAGTTGCGCGCCGC 100
Db 1 ATGGCGTTCGAGCAGGAGTGTGTATCGCGTGCACACCAAGGAGGAGTTGCGCGCCAC 60

Qy 101 ATGGCCAAAGGCGCAAGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 160
Db 61 ATGACCAAGGCGCAGGAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

Qy 161 AGTGGGTGCCAGATGATGCGCGCGCGGTGTACGGGACTGCGCGCAGGAGTACCTTCGCG 220
Db 121 GGTCCATGCCGCGCCATCGCCCACTGTCTCGAAACGCGCAAGAGTTCACCTCAGGTC 180

Qy 221 GTCTTCTCGAGGTCGAGTCGAGCAACTGTGGAAGTTCGGAAGATCTAGGCGTCCAT 280
Db 181 GTCTTCTGAAAGTGCAGGTCGAGCAAGTGAAGGAGTTCACCGCGGCTACGAGGTCGAG 240

Qy 281 GTGATGCCGACCTTCTGCTTCATCAGGAACGCGGAGCGCTCGAGAGCTTTGTACCGTC 340
Db 241 GCGATGCCGACCTTCCACTTGTCAAGAACGCGGAGCGGTCGCGACCATCGTGGGTGCC 300

Qy 341 GACGAGGACGAGCTCGGAGCGCGTCAAGGAGTACCGCGCGCTGGGACTTACGAGCGCT 400
Db 301 AGGAAGGACGAGCTCTGGCCCGAGATCGAGAAGCATGCGCGCGCTGGGCTGTGCG 360

Qy 401 CTTGCC 406
Db 361 TCTGCC 366

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Search completed: May 6, 2004, 03:45:14
Job time : 325.214 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 13:19:01 ; Search time 5435.21 Seconds
(without alignments)
10653.920 Million cell updates/sec

Title: US-10-005-429-24
Perfect score: 1336
Sequence: 1 gaactgaatttcagatttc.....cttagatatcaaaaaaaaaa 1336

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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14: gb_vi.*
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41: em_higo_ther.*

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1: gb_ba.*
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Pred. No. is the number of results predicted by chance to have a

RESULT 1
AK104317
LOCUS

DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full insert sequence.

ACCESSION AK104317.1 GI:32989526

VERSION FLI_CDNA; oligo capping.

KEYWORDS Oryza sativa (japonica cultivar-group)

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-length cDNA Consortium, National Institute of

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	809.8	60.6	1389	8	AK104317	AK104317 Oryza sat
2	808.2	60.5	1502	8	AK071251	AK071251 Oryza sat
3	755.4	56.5	1383	8	AK106368	AK106368 Oryza sat
4	730.2	54.7	1045	8	TA8421947	TA8421947 Triticum
5	709.6	53.1	118300	8	AP004165	AP004165 Oryza sat
6	708	53.0	1580	6	AX366999	AX366999 Sequence
7	684.4	51.2	1130	6	AX654214	AX654214 Sequence
8	683.4	51.2	131980	2	AP005477	AP005477 Oryza sat
9	623.4	46.7	963	6	AX653785	AX653785 Sequence
10	562.8	42.1	1021	6	AX366997	AX366997 Sequence
11	457	34.2	1152	6	AX507791	AX507791 Sequence
12	457	34.2	1152	6	AX651358	AX651358 Sequence
13	432.8	32.4	1433	8	BT004322	BT004322 Arabidops
14	421	31.5	1148	8	ATTHIRSDA	ATTHIRSDA A.thaliana
15	410	30.7	76170	8	AC002329	AC002329 Arabidops
16	404	30.2	1128	8	AY099756	AY099756 Arabidops
17	394.4	29.5	1261	8	ATTHIRSDA	ATTHIRSDA A.thaliana
18	390	29.2	27408	8	ATF15J1	ATF15J1 Arabidops
19	390	29.2	197859	8	ATCHRIV83	ATCHRIV83 Arabidops
20	335.4	25.1	1423	6	AR008096	AR008096 Sequence
21	333.8	25.0	1423	8	PCTRXB	PCTRXB Penicillium
22	321	24.0	2425	8	NEUCYS9	NEUCYS9 Neurospora
23	308	23.1	300425	1	AP005038	AP005038 Streptomy
24	301.2	22.5	303550	1	SC0939118	SC0939118 Streptomy
25	300.2	22.5	960	6	BD021847	BD021847 Thiodox
26	300.2	22.5	2592	8	SPU63713	SPU63713 Schizosacch
27	300.2	22.5	3058	8	AF535134	AF535134 Schizosac
28	300.2	22.5	17311	8	SPBC3P6	SPBC3P6 S.pombe c
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30	299.6	22.4	1898	1	SCTRXABGN	SCTRXABGN Streptomyce
31	293.2	21.9	4026	1	SC0007313	SC0007313 Streptomy
32	289	21.6	87340	1	AP005224	AP005224 Corynebact
33	283	21.2	13594	1	AE005952	AE005952 Caulobact
34	278.6	20.9	300200	1	AP005962	AP005962 Bradyrhiz
35	277.2	20.7	2134	8	SCU10274	SCU10274 Saccharomyc
36	275	20.6	12130	1	AE011416	AE011416 Leptospir
37	274.6	20.6	39954	8	YSCD8263	YSCD8263 Saccharomyc
38	272.8	20.4	349841	1	BX572606	BX572606 Rhodospheu
39	267.2	20.0	210205	1	AY223810	AY223810 Rhodococc
40	265.2	19.9	963	6	AX488837	AX488837 Sequence
41	262.8	19.7	1775	1	AF023161	AF023161 Mycobacte
42	261.2	19.6	963	1	SCTRXABGN	SCTRXABGN X92104 S.coelicolo
43	258	19.3	339650	1	AP003583	AP003583 Nostoc sp
44	257.6	19.3	1806	1	SCTRXABA	SCTRXABA Z21946 S.clavulige
45	256.2	19.2	951	6	AX123501	AX123501 Sequence

ALIGNMENTS

AK104317 1389 bp mRNA linear PLN 24-JUL-2003
Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full insert sequence.

AK104317

AK104317.1 GI:32989526

FLI_CDNA; oligo capping.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzoideae; Oryza.

REFERENCE 1

AUTHORS The Rice Full-length cDNA Consortium, National Institute of

Agrobiological Sciences Rice Full-Length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, E., Hotta, I.,
 Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuka, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group, Ohtsuka, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narioka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
 Saito, K., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from
 japonica rice
 Science 301 (5631), 376-379 (2003)
 27552273
 12869764
 2 (bases 1 to 1389)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,
 Hori, F., Hotta, I., Iida, J., Ikeda, R., Ishikawa, M., Itoh, M., Kagawa, I.,
 Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I.,
 Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
 Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
 Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Kurotsaki, T., Kusumegi, T., Li, C., Lu, M.,
 Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
 Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, N.,
 Namiki, T., Narioka, R., Niikura, J., Nishi, K., Nomura, K.,
 Numasaki, R., Ohneda, E., Ohno, M., Ohtsuka, K., Oka, M., Ooka, H.,
 Osato, N., Ota, Y., Ohtsuka, K., Ohtsuka, K., Sakai, C., Sakai, K.,
 Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
 Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
 Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
 Tagawa, A., Takahashi, P., Takaku-Akai, S., Tanaka, T., Tomaru, A.,
 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., and
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.
 Direct Submission
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
 Tel: 81-29-838-7007, Fax: 81-29-838-7007)
 This clone is one of the 28K full-length cDNA clones from japonica
 rice.
 URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuka, K., Shishiki, T. and
 Yamamoto, M.
 PALS Genome Sequencing & Analysis Group: Ohtsuka, K., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
 Niikura, J., Narioka, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
 Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
 Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Saeki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
 Takaku-Akai, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
 Yasunishi, A. and Hayashizaki, Y.
 Location/Qualifiers
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 /clone="001-024-C03"
 FEATURES
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 Query Match 60.6%; Score 809.8; DB 8; Length 1389;
 Best Local Similarity 80.8%; Pred. No. 1.8e-120;
 Matches 957; Conservative 0; Mismatches 227; Indels 1; Gaps 1;
 ORIGIN
 QY 87 AGCTATGAGGAGATCCCGCGCGCTTCCGCTCCGCAOCCGCGATCTGCATCTCGGAGCGG 146
 DB 104 AGCCATGAGGAGATCCCGCGCGCGCTCCGCAOCCGCGATCTGCATCTCGGAGCGG 163
 QY 147 TCCCGCTCGGCACACCGGAGGATCTAGCGCGCGCGCGCGGAGCTCAAGCTGTGCTCTT 206
 DB 164 GCGCTCGGCGGACACCGGCGGCGGATCTAGCGCGCGCGCGGAGGTCGAAGCGCTGCTT 223
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 QY 867 CAATTTCTTCCGCGGCGGAGCTTGAACCTGAGCTTGGGCAACAACATCTCTCGAGACCGCTT 926
 DB 884 GAAGTTTCTTCCGCGGCGGAGCTTGAACCTGAGCTTGGGCAACAACATCTCTCGAGACCGCTT 943

TITLE
 JOURNAL

COMMENT

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RESULT 2
 AK071251
 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) cDNA clone. J023087H21, full insert sequence.
 AK071251
 ACCESSION
 AK071251.1 GI:32981274
 VERSION
 FLI CDNA; CAP tripper.
 KEYWORDS
 Oryza sativa (japonica cultivar-group)
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 1
 AUTHORS
 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nami, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurokawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamura, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Iehi, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)

TITLE
 JAPONICA RICE
 MEDLINE
 22752273
 PUBMED
 12869764
 REFERENCE
 2 (bases 1 to 1502)
 AUTHORS
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawagashira, N., Kawai, J., Kawamura, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Kurokawa, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,

Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Omasaki, R., Ota, Y., Otsu, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sugabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yasaki, J., Yokomizo, S. and Yoshimura, A.
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 Tel: 81-29-838-7007, Fax: 81-29-838-7007
 This clone is one of the 28K full-length cDNA clones from japonica rice.
 URL: http://cdna01.dna.affrc.go.jp/cdna/

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nami, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ohtsuki, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamura, M., Kobayashi, M., Kodama, T., Kurokawa, R., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES
 Location/Qualifiers
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 Best Local Similarity 80.7%; Pred. No. 3.3e-120;
 Matches 956; Conservative 0; Mismatches 228; Indels 1; Gaps 1;

Qy 87 AGTATGGAGGATCGCGCGCTCGCTCGCGACGCGCATCTCATCATCGGAGCGG 146
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 Qy 147 TCCCGTGGCGACACGGGAGCCATCTAGCGCGCCCGCGGAGCTCAAGCTGTCTT 206
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1047 CTGCGAGGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1106
1080 TCTGCGAGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139
1107 CAGCAATCCATCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1166
1140 CACGAGGCTTCAAGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199
1167 GCGAGGCTTCAAGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1226
1200 GCGAGGCTTCAAGAGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1258
1227 TGCTATCTTATCGTTAGGCTCCGAGAGTATGCTGGAAGTCTGAA 1271
1259 TCGTATTTATGCTGCTGAGAGTTTATCTGTTATTTACGCTGAA 1303

RESULT 3
AK106368
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:002-102-C03, full insert sequence.
ACCESSION AK106368
VERSION AK106368.1 GI:32991577
KEYWORDS FLI_CDNA; oligo capping.

SOURCE
ORGANISM

REFERENCES
AUTHORS

TITLE
JOURNAL
MEDLINE
PUBMED

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team:
Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,
Kishimoto, N., Yabuchi, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
Kojima, K., Nishikawa, S., Ohneda, E., Yabuchi, M., Suzuki, K., Li, C.,
Chen, K., Shihiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group, Otsu, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiya, A., Mizuno, K., Yokomizo, S., Nishikawa, J.,
Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryū, R., Ueda, M., Matsubara, K., RIKEN,
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, F., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Otsu, N., Ota, Y.,
Saito, K., Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Yoshino, M., and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from
Japonica rice
Science 301 (5631), 376-379 (2003)
2752273
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2 (bases 1 to 1383)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, N.,
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Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,
Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M.,
Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koyda, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
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Nami, T., Narikawa, R., Nishikawa, J., Nishi, K., Oka, M., Ooka, H.,
Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Sakai, C., Sakai, K.,
Sato, N., Ota, Y., Otsu, Y., Ryū, R., Saitoh, H., Sakai, C., Sakai, K.,
Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K.,
Shingawa, A., Shiraki, T., Shihiki, T., Sogabe, Y., Sugano, S.,
Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y.,
Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,
Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yabuchi, M.,
Yamada, H., Yamamoto, M., Yasunishi, A., Yabuchi, J., Yokomizo, S. and
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305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yabuchi, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishikawa, T.,
Ohneda, E., Yabuchi, M., Suzuki, K., Li, C., Ohtsuki, K., Shihiki, T. and
Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryū, R., Sugano, S.,
Sugiyama, A., Suzuki, K., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
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ORIGIN	7C10HNE=002-102-C03									
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ORIGIN

Query Match 54.7%; Score 730.2; DB 8; Length 1045;
 Best Local Similarity 82.8%; Pred. No. 1.2e-107;
 Matches 834; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 91 ATGAGGAGATCCGCGCGCGCTCCGCTCCGCGACGGCGATCTGCATCATCGGAGCGTCCC 150
 DB 38 ATGAGGAGGCGCGCGCGCGCTGTCACACGGCGGTGTCATCATTCGGAGCGGCC 97

QY 151 GCTGCGACACGGAGCATCTACCGCGCGCGCGCGAGCTCAAGCTGTGCTTCGAG 210
 DB 98 GCGCGGACACGGCGCGCTTACCGCGACGGCGCGAGCTCAAGCGCGCTTCGAG 157

QY 211 GCGTGGATGGCCAAACAGATCGCGCGCGCGCGAGCTCACACACACCGAGCTCGAG 270
 DB 158 GCGTGGCTCGCAACAGATCGCGCGCGCGCGAGCTCACACACACCGAGCTCGAG 217

QY 271 AACTTCGCGGCTTCCCAACGGGATCATGGCGCGCGAGCTCATGACCACTGCGCGCG 330
 DB 218 AACTTCGCGGCTTCCCGGAGGATCTCTCGGATTCGACCTCATGAGACCGTGGCGCG 277

QY 331 CAGTCCCTCGGCTTGGCACCAATCTCTCCGAGACCGTCAACCGCGCTGCTTCG 390
 DB 278 CAGTCCGTCGCTTGGGACCAAGATCTCTCCGAGACCGTCACTCTCGCTGCTTC 337

QY 391 GCTTCGCTTCGAGTGTAGTGCAGATCTCAACACCGTCTCCGCGAGTGGCTTACGTT 450
 DB 338 TCCGCGCTTCCGCGCTCTCTCCGAGACACCGTCTCGACCGCGCTCGTGTGTC 397

QY 451 GCCAGGAGCGCTCGCGCGCGCTTCACTTCCCGCGGTCCGATGATGATGACCGC 510
 DB 398 GCCACCGCGCGCTCGCGCGCGCTTCCATCTTCGCGGCTCCGACGCGTTCGACCGT 457

QY 511 GGCATCTCGGCTGTCGCGGTGCGCGCGCGCTTCCGATGATGATGATGATGATGATG 570
 DB 458 GGGATCACCGCTGCGCGCTGCGCGCGCGCTTCCGATGATGATGATGATGATGATG 517

QY 571 GCGGTATAGGCGCGCGCTCGCTATGAGGAGTCCAAATTTCTTCCACCAAGTACGCG 630
 DB 518 GCGGTGCTGCGTGGCGGAGCTTCCCATGAGGAGGCAACTTCTTCCACCAAGTACGCG 577

QY 631 TCCACGCTCATCATCATCGCGCGCGCTTCCGATGATGATGATGATGATGATGATG 690
 DB 578 TCGCGGCTTACATCATCATCGCGCGCGCTTCCGATGATGATGATGATGATGATG 637

QY 691 AGGCGCTTGAACCCCAAAATTAAGTCTCTGGGACTCGGAGTGTGCGAGGCTAT 750
 DB 638 CCGGCTCTCTCAACCCCAAAATCCAGGTCTGTGGGACTCCGAGTGTGCGAGGCTAC 697

QY 751 GCGCGGCAACCGCGCGCGCTTGGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 810
 DB 698 GCGGCTTGGAGCGCGCGCGCTTGGGCGGCTTGAAGTGAAGTGAAGTGAAGTGAAG 757

QY 811 GTCGCTGATCTTCAAGTGTCTGCGCTTCTTCCGATGCGGATGCGCGCGCGCAAA 870
 DB 758 GTATCCGATCTTCCGCTGCGCGCTTCTTCTTCCGATGCGGATGCGCGCGCGCAAA 817

QY 871 TCCCTGGCGGACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 930
 DB 818 TTTCTCGCGGACGCTGAGCTGATCTCGAGGAGTACGTTGGCCCAAGCGCGGCTCC 877

QY 931 ACTCAACAGTGTAAAGGCTGTATTTCTGCTCTGCGAGCGTGCAGGACAAAGATACCGT 990

DB 878 ACCGACACAGTGTGAGGGGGTCTTCGCTCGCGGAGCGTTCCAGGACAAAGTACCGC 937

QY 991 CAGGCGATTAAGTGTGAGTCAAGGTGATGCTGCTGATGAGCGTCAAGTCAAGTCAAGT 1050

DB 938 CAGGCGATTAAGTGTGAGTCAAGGTGATGCTGCTGATGAGCGTCAAGTCAAGTCAAGT 997

QY 1051 CAGGAGATCGGTGACACAGGAGGAAAGTCTGATGAGTATATATTTAGG 1097

DB 998 CAGGAGGTGTGGCGACAGGAGGCAAGTCAATGACTATATGTGG 1044

RESULT 5
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 LOCUS
 DEFINITION
 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
 BAC clone:OJ1479_B12, complete sequence.
 ACCESSION
 AP004165
 VERSION
 AP004165.2 GI:34447188
 KEYWORDS
 HTG
 SOURCE
 Oryza sativa (japonica cultivar-group)
 ORGANISM
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

1
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
 clone:OJ1479_B12
 Published Only in Database (2001)
 2 (bases 1 to 118300)
 Sasaki, T., Matsumoto, T. and Yamamoto, K.
 Direct Submission
 Submitted (12-SEP-2001) Takuji Sasaki, National Institute of
 Agrobiological Sciences, Rice Genome Research Program, Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 Tel:81-298-38-7441, Fax:81-298-38-7468)
 On Sep 3, 2003 this sequence version replaced gi:15594177.
 The orientation of the sequence is from M13rev to -21M13 of the BAC
 clone. The nucleotide sequence of this BAC clone was generated by
 combining Monsanto and RGP-Japan sequencing data.

FEATURES
 Location/Qualifiers
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 /chromosome="2"
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ORIGIN

Query Match 53.1%; Score 709.6; DB 8; Length 118300;
 Best Local Similarity 85.1%; Pred. No. 1.4e-104;
 Matches 793; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 87 AGCTATGAGGAGTCCCGCGCTCCGCAACCGCATCTGCGCATCTGCGAGCGG 146

DB 99810 AGCCATGAGGAGTCCCGCGCGCGCTCCGCAACCGCATCTGCGAGCGG 99751

QY 147 TCCCGTCCGCGACAGCGCATCTACGCGCGCGCGCGAGCTCAAGCTGTGCTTT 206

DB 99750 GCGGTCCGCGACAGCGCGCGCATCTACGCGCGCGCGCGAGCTCAAGCTGTGCTTT 99691

QY 207 CGAGGCTTGAATGCCAAACGACATCGCGCGCGCGCGAGCTCACCAACCGAGCT 266

DB 99690 CGAGGCTTGAATGCCAAACGACATCGCGCGCGCGCGAGCTCACCAACCGAGCT 99631

QY 267 CGAGGACTTCCCGCGCTTCCCAACCGCATCTGCGCGCGCGAGCTCATGACAACTGCCG 326

DB 99630 CGAGGACTTCCCGCGCTTCCCAACCGCATCTGCGCGCGCGAGCTCATGAGTCCGTCG 99571

QY 327 CGCGAGTCCCGCTGCTTGGCAACATCTCTCCGAGACCGTCAACCGCGCTTCACTT 386

785 GCGGTCCGTTGGCGCGCTCAAGAACGTGGTGAAGCGCGGAGGTCTCCGACCTCC 844

824 AGGTGTCGGGCTCTCTCTTCGGCATCGGCGACCGCGGACCAAAATTCCTGGGGGAC 883

845 AGGTGCGCGGGCTCTCTTCGGCATCGGCGACCGCGGACCAAAATTCCTGGGGGAC 904

884 AGCTTGAATCCGATTCAGATGGTTATGTGGAACCAAGCCAGGTTCCTCATCACCAGTG 943

905 AGCTCGAGCTGAGCTTCGATGGCTATGCTGACCAAGCCCGGCTCCACTCATCACCAGCG 964

944 TAAAGGTTGATTGCTGCTCGGACGTCGACGACAGAAAGTACCGTCAGGCGATTACTG 1003

965 TCAAGGAGTCTTCGCGCGGCTGATGTTTCAGGACAAAGAAATATCGCCAGGCCATTACTG 1024

1004 CGCTGGATCAGGGTGCAATGGCTGCATTGG 1033

1025 CCGGGATCAGATCGAAGACATTACAGG 1054

RESULT 8

AP005477

LOCUS

DEFINITION

AP005477 131980 bp DNA linear HTG 28-JUN-2002

OSJNB0039F24, ** SEQUENCING IN PROGRESS ***.

AP005477

HTG; HTGS PHASE2.

ACCESSION

AP005477.1 GI:21624397

VERSION

AP005477.1

KEYWORDS

ORIGIN

ORIGIN

ORIGIN

Query Match 51.2%; Score 683.4; DB 2; Length 131980;

Best Local Similarity 81.4%; Pred. No. 2.2e-100;

Matches 792; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

44 CCACCGCGCGCGCGCGGACCGAAGCCAGCCAAACTGATGACGAGGATCGAGGATCCG 103

82586 CCGCGCGCTCCGGTTCAGTCGACGCGCGCGCGCGCGTGGCGAAGCGGATCGAGGCGG 8264

QY 871 TTCTGGCGGACAGCTTGAACCTCGATTCAGATGGTTATGTGAAACCAAGCCAGGTTC 930
DB 745 TTTCTGGCGGCGAGCTTGAACCTCGATTCAGATGGTTATGTGAAACCAAGCCAGGTTC 864
QY 931 ACTCACACAGTGTAAAGGTGTATTGCTGCTGGGACGCTGAGCAGCAGAGATACCT 990
DB 805 ACGCACACAGTGTAAAGGTGTATTGCTGCTGGGACGCTGAGCAGCAGAGATACCT 864
QY 991 CAGGCCATTACTGCCGCTGGATCAGGCTGCA 1021
DB 865 CAGGCTATTACTGCCGCTGGATCAGGCTGCA 895
RESULT 10
AX366997
LOCUS 1021 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 24 from Patent WO0198509.
ACCESSION AX366997
VERSION AX366997.1 GI:18698274
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
Lanahan,M.B., Desai,N.M. and Gasdaska,P.Y.
Grain processing method and transgenic plants useful therein
Patent: WO 0198509-A 24 27-DEC-2001;
Syngenta Participations AG (CH)
FEATURES
source
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ORIGIN
Query Match 42.1%; Score 562.8; DB 6; Length 1021;
Best Local Similarity 74.2%; Pred. No. 9e-81;
Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;
QY 113 CGTTCGCGACGCGCATTCGATCATATCGGAGCGGTCCGCTGGCGACACGGAGCCATCT 172
DB 26 CTCACACACCGCGCTTCGATCGTTGGCTCCGCGCGGCTGCCACACCGCGCCATCT 85
QY 173 ACGCGCGCGCGGAGCTCAAGCTCTGCTTCGAGGCGTGGATGGCCACACGACATCG 232
DB 86 ACGCGCGCGCGGAGCTCAAGCTCTGCTTCGAGGCGTGGATGGCCACACGACATCG 145
QY 233 CCGCGCGCGCGGAGCTCAACACACACACGCTCGAGAACTTCGCGGCTTCCCAACG 292
DB 146 CCGCGCGCGGAGCTCAACACACACGCTCGAGAACTTCGCGGCTTCCCAACG 205
QY 293 GCATCAGGCGCGGAGCTCAAGCTCTGCTTCGAGGCGTGGATGGCCACACGACATCG 352
DB 206 GCATCAGGCGCGGAGCTCAAGCTCTGCTTCGAGGCGTGGATGGCCACACGACATCG 265
QY 353 ACATCTCTCCGAGACCGCTCACCGCGCTCGACTTTTCGGCTGCCATTCGCGGCTTAGTG 412
DB 266 CCATCTTCAGGAGCGCTGACCAAGCTGACATTCGAGCAAGCGCTTCAAGCTCTTCA 325
QY 413 CAGACTCCACAAACGCTCTCGCGATGCGGTTATCGTTGCGACGGAGCGCTCGCGGCG 472
DB 326 CCGACTCCAAAGGCGCATCTCGCGACCGCGTGTCTCTGCGCATGCGCGCGTGGCCAAAGT 385
QY 473 GCTTCCACTTCCCGGGTC-----CGATGCATACTGGAACCGCGGATCTTCGCG 520
DB 386 GGTCTCTCTGCGGCTTCGCGGAGGTGCTCGCGGACCTCTGGACCGCGGATCTCGG 445
QY 521 CCGTGGCGGCTGGAAGCGGTCCCGCCCATCTTCGCTTAACAGCCCATGCGCGTATAG 580
DB 446 CCGTGGCGGCTGGAAGCGGTCCCGCCCATCTTCGCTTAACAGCCCATGCGCGTATAG 505

QY 581 GCGGCGGCGACTCCGCTATGAGAGAGTCCAAATTTCTCTACCAAGTACGGCTCCAGGTCT 640
DB 506 GTGCGGAGACAGCGCGATGAGAGAGGCGCAATTTCTCTACCAAGTACGGCTCCAGGTCT 565
QY 641 ACATCATCCACGCGCGCAATACCTTTCCGTCTTCAAGATCATGAGGCGCGGCGCTTG 700
DB 566 ACATCATCCACGCGCGCGCAATACCTTTCCGTCTTCAAGATCATGAGGCGCGGCGCTTG 625
QY 701 AGAAGCCCAAAATTAAGGTCCTCTCGGACTCGGAAGTTGTTCAGGCGCTTAGCGGCGAA 760
DB 626 CCAAGCCGAAGATCGACGCTCATCTCGAACTCTCTCGGTGTGAGGCGCTACCGCGCAAGCG 685
QY 761 ACGGCGCGCCATTGCGTGGCTGCTAAGAGTTAAGAACTCTGATGTTGAGGCTCTCGATC 820
DB 686 ACGGCGCGCCATTGCGTGGCTGCTAAGAGTTAAGAACTCTGATGTTGAGGCTCTCGATC 745
QY 821 TTGAGGTGTCTGCGCTCTTTCTTCGCCATCGGCGCATAGCCGCGCACCAAAATTTCTTGGGCG 880
DB 746 TCAAGGTGTCTGCGCTCTTTCTTCGCCATCGGCGCATAGCCGCGCACCAAAATTTCTTGGGCG 805
QY 881 GACAGCTTGAACCTCGATTCAGATGTTATGTAACCAACCAAGCGAGTTTCACTCACCA 940
DB 806 GCGGCGTGGAGTGGACTCCGACGCTAGTGGTGACCAAGCGCGGCGCACCCAGACTT 865
QY 941 GTGTAAGGCTGTATTGCTGCTGCGAGCTGCAGGACAAAGTACCGTCAAGGCGCATTA 1000
DB 866 CCGTGCCTGGCTGTTCGCGCGCGGAGCTGCAGGACAAAGTACCGGCGGCGCATCA 925
QY 1001 GTGCGCGTGGATCAGGCTGCTGCTGATTTGAGCTGAGCAGCTGAGCAGCTTACCTGAGGAGATCG 1060
DB 926 CCGCGCGCGCGCACCGCGCTGCTGCGCGCGCTGAGCTGAGCAGCTGAGCAGCTTACCTGAGGAGATCG 985
QY 1061 GTGCAAGGAGGGAAGTCTGATT 1084
DB 986 GCTCCAGCAGGCGGAGTCTCGACT 1009
RESULT 11
AX507791
LOCUS 1152 bp DNA linear PAT 27-SBP-2002
DEFINITION Sequence 2486 from Patent WO0216655.
ACCESSION AX507791
VERSION AX507791.1 GI:23389028
KEYWORDS Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 2486 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)
FEATURES
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1..1152
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/mol_type="unassigned DNA"
/db_xref="taxon:3702"
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Query Match 34.2%; Score 457; DB 6; Length 1152;
Best Local Similarity 67.9%; Pred. No. 8.8e-64;
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;
QY 128 TCTGATCATTCGGAGCGGTCCGCTGCGCACACGAGCCATCTACGCGGCGCGCGG 187
DB 182 TTTGATCTCGAAGTGGACACGAGCAGCACACGCGCGGCTATGATCATCGAGAGCGG 241
QY 188 AGCTAAGCTCTGCTCTTCGAGGCGTGGATGCGCACGATCGCGCGGCGGCGACG 247


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Db      962 ATGAAGATGGTATTGTTGTGACCAAGCCAGGTACTACTAAGACGAGCGTGGTGGTGTAT 1021
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Db      1022 TTGCTGCTGGAGATGTTCAAGACGAAGATATACACAGGCGCATCACTGCTGCGAGAACTG 1081
Qy      1016 GGTGCATGGCTGCTGAGTGGACCTGAGCACTACCTGCGAGGAGATCGGTGCGACAGAGGAA 1075
Db      1082 GGTGCATGGCGGCAATGGATGACAGAGCATTAATTAAGAGATGGATCTCAGGAGGGTA 1141
Qy      1076 AGTCTGATTGA 1086
Db      1142 AGAGTGATTGA 1152

RESULT 13
BT004322
LOCUS   Arabidopsis thaliana clone RAFL16-02-L06 (R50174) putative
DEFINITION thiorodoxin reductase (NADPH) 2 (At4g35460) mRNA, complete cds.
ACCESSION BT004322.1 GI:28393818
VERSION    1
KEYWORDS  FLI CDNA.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1433)
AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
           Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
           Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
           Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
           Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
           Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
           Ecker,J.R. and Theologis,A.
TITLE     Arabidopsis Full Length cDNA Clones
JOURNAL   Unpublished
REFERENCE 2 (bases 1 to 1433)
AUTHORS   Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M.,
           Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,
           Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y.,
           Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,
           Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,
           Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,
           Ecker,J.R. and Theologis,A.
TITLE     Direct Submission
JOURNAL   Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan
           Street, Albany, CA 94710, USA
COMMENT   RIKEN Genomic Sciences Center (GSC) members carried out the
           collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
           Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
           Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
           Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGECC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M.,
Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Chodera,C.S.,
Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G.,
Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,
Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,
Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGECC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGECC)
contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome
submitted to Genbank
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/notes="This clone is in a modified pBluescript vector2
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Matches 654; Conservative 0; Mismatches 332; Indels 12; Gaps 1;
Qy 108 CGCTCCGCTCCGACACGCGCATCTGCATCATCGGGAGGGTCCCGCTCGGCACACGCGCAGC 167
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Qy 168 CATCTACGCGGCGCGCGCGGAGCTCAAGCCTGTGCTCTTCGAGGGCTGGATGCGCACGA 227
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Qy 228 CATCGCGCGGCGCGCGCGAGCTCAACACCGACGTCGAGAACTTCCCGGCTTCCC 287
Db 205 CATCGCTCCGCTGGTCAACTACACACCGACGTCGAGATTTCCCGGATTTCC 264
Qy 288 CAACGCGCATATGGCGCGCGAOCCTCATGACAACTCCCGCGCGCAGTCCCTTGGCTTGG 347
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Qy 348 CACCAACNTCTCTCCGAGACCGTCAACCGCTGCGATTTTGGCTGCGCATTCGAGT 407
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Qy 408 TAGTGCAGACTCTCAACACCGTCTCCCGATGCGGTATATGTTGCCACGCGAGCGCTGCG 467
Db 385 ATTACAGAGATTCAAAAGCCATTCTCGCTGACGCTGATTTCTGCTACTGAGAGCTGTGG 444
Qy 468 GCGCGCTCTCACTTCCCGGCTCCGATGCA-----TACTGGAAACCGGCGCAT 515
Db 445 TAAGCGGCTTAGCTTCGTTGGATCTGGTAGGCTTCTGAGAGTTCTGGACCGTGAAT 504
Qy 516 CTCGCGCTGTGCGCTGTGTGACGCTGCGCGCCCGCCCATCTTCCGTTAAACGCCCATCCGCT 575
Db 505 CTCGCTGTGTGCTGTGTTGGCGGAGCTGCTCGATATTCGTTAAACAACTCTTGGCT 564
Qy 576 CATAGCGCGCGCGAGCTCCGCTATGAGGAGTCCATTTCTTCTCACCAGTACGCTCCCA 635

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Db 565 GATCGTGGGCGGATTCAGCAATCGAAGACCAACCTCTTACAAATATGATCTAA 624
Qy 636 CGTCTACATCATCCACCGCCGATACCTCTCGTCTCCAGATCATGCGAGCCAGGCC 695
Db 625 AGTGTATATAATCCATAGGAGATGCTTTTAGAGCGCTAAGATATATGACGACCGGAGC 684
Qy 696 GCTTGAGAACCCCAAAATTAAGTCTCTGCGGATCTCGGAGCTTTCGAGGCTATGGCGG 755
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Qy 1056 GATCGTGCACAGGAGGAAAGTCTGATGACTATATT 1093
Db 1045 GATTGGATCTCAGCAAGGTAAAGTGAATGAGAAATT 1082

RESULT 14
LOCUS ATTHIREDA 1148 bp mRNA linear PLN 25-MAR-1994
DEFINITION A.thaliana mRNA for NADPH thioredoxin reductase.
ACCESSION 223108
VERSION 223108.1 GI:468523
KEYWORDS NADPH thioredoxin reductase.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 1148)
JACQUOT, J.P., RIVERA-MADRIG, R., MARINHO, P., KOLLAROVA, M., LE
MARECHAL, P., MIGNINIAC-MASLOW, M. and MEYER, Y.
Arabidopsis thaliana NADPH thioredoxin reductase. cDNA
characterization and expression of the recombinant protein in
Escherichia coli
J. Mol. Biol. 235 (4), 1357-1363 (1994)

JOURNAL MEDLINE
PUBMED 8308900
REFERENCE 2 (bases 1 to 1148)
Meyer, Y.
Direct Submission
Submitted (24-JUN-1993) Yves Meyer, Labo de Physio et Biol Mol
Vegetales, CNRS, URA 565, Av. de Villeneuve, PERPIGNAN, 66860,
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CDS
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Qy 308 ACCTCATGGAACACTCGCGCGCGAGTCCCTGCGCTTTGGCACCACCAATCATCTCTCCGAGA 367
Db 121 ATATCGTTGAGAAATTCAGAAACAATCGGAGAGATTGGAACTACGATCTTCAGGAAA 180
Qy 368 CCGTCACCGCGCTCGACTTTTTCGCGCTCCCAATTCGAGTTAGTCAGACTTCCCAACCG 427
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Qy 428 TCCTCGCGGATGCGGTTATGCTTCGCGAGGCGCTGCGGCGGCGCTCCACATTCGCCG 487
Db 241 TTCTCGCTGATTCGTAAATCATTTCTACTGAGCTGTGTCTTAAACGCTTAGCTTCACTG 300
Qy 488 GGTCCGATGCA-----TACTGGAAACCGCGCATCTCCGCTCTGTCGCTGTG 535
Db 301 GATCTGTGGAAGTAATGGTGTGTTTGGATCGTGTATCTCCGTTGCTGTGTTGCG 360
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Db 721 ATGAAGATGGTTATGTTGTGACCAAGCCAGGCTACTTACTAAGACGAGCTGGTGGTGTAT 780
Qy 956 TTGCTGCTGGCGAGCGTGCAGGACAGAAAGTACCGTCAGGCCCATTTACTCCGCTGCATCAG 1015
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QY 1016 GGTGATGCTGATGAGCGTGGACCTACCTGACAGAGATCGGTGACAGAGGAA 1075
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 QY 1076 AGTCTGATTGA 1086
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RESULT 15
 AC002329 76170 bp DNA linear PLN 05-APR-2000
 Arabidopsis thaliana chromosome II section 100 of 255 of the
 complete sequence. Sequence from clones T23A1, F5J6, MJB20.

ACCESSION AC002329
 VERSION AE002093
 KEYWORDS
 SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 76170)
 Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,
 Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,
 Feldlyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Renning, C.M.,
 Xoo, H., Moffatt, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L.,
 Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,
 Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,
 Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and
 Venter, J.C.

TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana

JOURNAL Nature 402 (6763), 761-768 (1999)
 MEDLINE 20083487
 PubMed 10617197

REFERENCE 2 (bases 1 to 76170)
 Lin, X.

TITLE Direct Submission
 JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 On Dec 17, 1999 this sequence version replaced gi:2262155.
 The sequence and annotation of chromosome 2 were merged from those
 of the individual clones on this chromosome after removing
 overlaps. For detailed information, please see the TIGR web site
 (<http://www.tigr.org/tcdb/at/at.html>).

Genes were identified by a combination of three methods: Gene
 prediction programs including GRAIL
 (<ftp://arthur.epm.ornl.gov/pub/xgrail>), GeneFinder (Phil Green,
 University of Washington), Genscan (Chris Burge,
<http://gnomic.stanford.edu/GENSCANW.html>), and NetPlantGene
 (<http://www.cbs.dtu.dk/services/NetGene2/>), searches of the
 complete sequence against a peptide database and plant EST
 databases at TIGR, and manual curations based on these analyses.
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as 'unknown' proteins.
 Genes without protein or EST similarity, that are predicted by two
 or more gene prediction programs over most of their length are
 annotated as 'hypothetical' proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats were
 identified by RepeatMasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are
 numbered from the top to bottom of the chromosome.

We thank the CSHL/WashU/ABI consortium for sequencing BAC clones
 F623, F5J6, T17A5, and T31B1, the ESSA group for sequencing clone
 F13B4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards
 and Satoshi Tabata for helpful assistance. In addition, we would
 like to thank the TIGR Bioinformatics Department, especially Tixi

Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy
 Peterson, Michael Holmes, and Delwood Richardson for software and
 database support.

This work was supported by the National Science Foundation,
 Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

FEATURES

source

Location/Qualifiers
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 03:32:20 ; Search time 592.538 Seconds

(without alignments)
9578.440 Million cell updates/sec

Title: US-10-005-429-24

Perfect score: 1336

Sequence: 1 gaactgaatttcagatttc.....cttagatatcaaaaaaaaaa 1336

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002s.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	757.6	56.7	1391	3 AAC62460	AAC62460 Barley NA
2	708	53.0	1560	6 AAD29838	AAD29838 Rice NADP
3	684.4	51.2	1130	7 ADA70761	ADA70761 Rice gene
4	623.4	46.7	963	7 ADA70332	ADA70332 Rice gene
5	562.8	42.1	1021	6 AAD29837	AAD29837 Arabidops
6	457	34.2	1152	3 AAC43307	AAC43307 Arabidops
7	457	34.2	1152	6 AB214681	AB214681 Arabidops
8	457	34.2	1152	7 ADA67905	ADA67905 Arabidops
9	457	34.2	1152	3 AAC48213	AAC48213 Arabidops
10	440.6	33.0	6357	9 AAL54488	AAL54488 Thioresox
11	440.6	33.0	6357	9 AAD26526	AAD26526 Thioresox
12	435.8	32.6	6357	7 AAL54493	AAL54493 Thioresox
13	435.8	32.6	6357	9 AAD26531	AAD26531 Thioresox
14	435.8	32.6	6357	9 AAD26533	AAD26533 Thioresox
15	434.6	32.5	1313	3 AAC34825	AAC34825 Arabidops
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22	432.8	32.4	1539	3 AAC36511	AAC36511 Arabidops
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24	432.6	32.4	6357	7 AAL54484	AAL54484 Thioresox
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28	432.6	32.4	6357	9 ADD26522	ADD26522 Thioresox
29	432.6	32.4	6357	9 ADD26523	ADD26523 Thioresox
30	431.8	32.3	3787	6 ABN89582	ABN89582 Phaseolin
31	431.8	32.3	3787	6 ABS53098	ABS53098 cDNA enco
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33	431.8	32.3	4546	6 ABS53099	ABS53099 DNA encod
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35	431	32.3	6357	7 AAL54491	AAL54491 Thioresox
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38	431	32.3	6357	7 AAL54487	AAL54487 Thioresox
39	431	32.3	6357	9 ADD26525	ADD26525 Thioresox
40	431	32.3	6357	9 ADD26517	ADD26517 Thioresox
41	431	32.3	6357	9 ADD26534	ADD26534 Thioresox
42	431	32.3	6357	9 ADD26527	ADD26527 Thioresox
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44	431	32.3	6408	7 AAL54482	AAL54482 Thioresox
45	430.8	32.2	4545	6 ABN89584	ABN89584 Phaseolin

ALIGNMENTS

RESULT 1

AAC62460 AAC62460 standard; DNA; 1991 BP.

AC AAC62460;

DT 07-FEB-2001 (first entry)

XX Barley NADPH-thioresoxin reductase coding sequence.

XX Barley; NADPH-thioresoxin reductase; disulfide bridge reduction; NTR; development; thioresoxin h; hair care product; venom neutralisation; food technology; food allergy; ds.

OS Hordeum vulgare.

PN WO200058352-A2.

XX PD 05-OCT-2000.

XX PF 31-MAR-2000; 2000WO-US008566.

XX PR 31-MAR-1999; 99US-0127198P.

XX PR 06-DEC-1999; 99US-0169162P.

XX PR 21-JAN-2000; 2000US-0177739P.

XX PR 21-JAN-2000; 2000US-0177740P.

XX (REGC) UNIV CALIFORNIA.

XX Cho M, Del Val G, Caillaud M, Lemaux PG, Buchanan BB;

XX WPI: 2000-679291/56.

XX P-PSDB; AAB29250.

XX Recombinant or isolated nucleic acid, useful for producing transgenic plants with altered redox properties, encode thioresoxin h or thioresoxin reductase.

XX Claim 66; Fig 5B; 125pp; English.

XX The present invention relates to the isolation and use of the barley thioresoxin h and NADPH-thioresoxin reductase coding and protein sequences. Thioresoxin is thought to be involved in plant development via its function in the reduction of disulfide bridges. Thioresoxin can be used in hair care products and in the neutralisation of some venoms and toxins, and is also useful in the reduction of some food, for example it

Db 462 GCCGTGGGCGACACGGGGGGGATCTAGCCGCCCGGGGGAGCTCAAGCCCGTGTCTTT 521
Qy 207 CGAGGGCTGGATGCCCAACGACATCGCGCGGGGGGAGCTCAACCAACCAACCGACGT 266
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Qy 327 CGCGCAGTCCCTGCGCTTTGGACCAACATCTCTCGGAGACCGCTCAACCGCGCTGACCTT 386
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Qy 387 TTGGCTGCGCCATTCGAGTTAGTGAGACTCCACAAACCGTCTCGCGGATCGGTTAT 446
Db 702 CTGCGCGCGCGCTTCTCGCTGCGCTCGACTCCACCAACCGTCTCGCGGAGCGGCTG 761
Qy 447 CGTTGCCAAGGAGCGCGCGCGCTTCCACTTCCCGGGGCTCGATGCATCACTCGAA 506
Db 762 CGTGCACACCGCGCGCTTCCCGCGGACTTCACTTCCCGGGCTCGAGCGCTACTCGAA 821
Qy 507 CGCGGCACTCCCGCTGTGCGCTGTGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 566
Db 822 CGCGGCACTCCAGCTGCGCGCTTGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 881
Qy 567 CATCGCGCTATAGCGCGCGCGCTCGCTATCGAGAGTCCATTTCTTCCACCAAGTA 626
Db 882 CATCGCGCTATCGCGCGCGCGCTCGCTATCGAGAGTCCATTTCTTCCACCAAGTA 941
Qy 627 CGGCTCCCACTGACATCATCCACCGCGCGCAATCTTCCGTCTTCCAAAGATCATGCA 686
Db 942 CGGCTCCCACTGACATCATCCACCGCGCGCAACACTTCCCGCGCTTCCAAAGATCATGCA 1001
Qy 687 GCGCAGGCGCTTGGAAACCCCAAAATTAAGTCTCTGGGACTCGGAGTGTGAGGC 746
Db 1002 GCGCAGGCGCTTGGCAACCCCAAGATCCAGGTTTCTGGGACTCTGAGGTCGTGAGGC 1061
Qy 747 CTATGGCGCGCAACCGCGCGCGCTTGGCTGAGGTAAGGTTAAGAACCTTACTGAATGG 806
Db 1062 CTACGGCGCGAGGTTGAGGTCATTTGGCTGGTCTAAGTGTGAGAACTTGGTTACTGG 1121
Qy 807 TGAGGCTTCGATCTTCAAGTGTCTTCTTCTGCGCATCGGGCATGAGCGCGGAC 866
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Db 1182 GAAGTTTCTGCGCGGCGAGCTTGAACCTGATGCTGATGCTGATGCTGATGCTGATGCT 1241
Qy 927 TTCCACTCACACCAAGTGTAAAGGTTGTTATTTGCTGCTGCGCAAGTGTGAGGAAAGTA 986
Db 1242 CTCCACGACACCAAGTGTAAAGGTTGTTATTTGCTGCTGCGGATGTGCAAGGAAAGTA 1301
Qy 987 CGGTGAGGCCATTACTCGCGCTGATCAGGTT 1018
Db 1302 TCGCCAGGCTATTACTGCGCTGGATCAGGTT 1333

RESULT 3

ADA70761

ID ADA70761 standard; DNA; 1130 BP.

XX

AC ADA70761;

XX

DT 20-NOV-2003 (first entry)

XX

DE Rice gene, SEQ ID 4084.

XX

KW Plant; bacterial infection; fungal infection; viral infection; rice;

XX

KW Gene; ds.

XX

OS Oryza sativa.

XX FN WO2003000898-A1.
XX PD 03-JAN-2003.
XX PP 22-JUN-2001; 2001WO-IB001105.
XX PR 22-JUN-2001; 2001WO-IB001105.
XX PA (SYN) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX Claim 6; SEQ ID NO 4084; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.

XX SQ Sequence 1130 BP; 174 A; 419 C; 358 G; 179 T; 0 U; 0 Other;

Query Match 51.2%; Score 684.4; DB 7; Length 1130;

Best Local Similarity 80.7%; Pred. No. 3.7e-146;

Matches 799; Conservative 0; Mismatches 191; Indels 0; Gaps 0;

Qy 44 CCACCG 103
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Qy 104 CGCGCGCTCGCTCG 163
Db 125 CG 184
Qy 164 CAGCATCTACCG 223
Db 185 CGCGCGCTTCAGCG 244
Qy 224 ACACATCTCG 283
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Qy 284 TCCCAACG 343
Db 305 TCCCGGCG 364
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Db 365 TCGGACCGAGATCTCTCAACCGAGACCGTCAACCGCGCGCGCGCGCGCGCGCGCG 424
Qy 404 GAGTAGTGAGACTCCACAAACCGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463
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Db 485 TCGCGCGCGCGCTCCACTTTCGCGGCTCCGCGCGCTTCTGGAACCGCGCGCGCG 544
Qy 524 GTGCGGCTCTGTGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583

QY 931 ACTCACACCAAGTGAAGAGGTGATTTGCTGCTGGGACCTGACGACCAAGAAGTACCTT 990
 DB 805 ACGCACACCAAGTGAAGAGGTGATTTGCTGCTGGGATGACGACCAAGAAGTATCC 864
 QY 991 CAGGCCATTACTGCGCTGGATCAGGCTGCA 1021
 DB 865 CAGGCTATTACTGCGCTGGATCAGATCA 895

RESULT 5

AAD29837
 ID AAD29837 standard; DNA; 1021 BP.

AC AAD29837;

DT 17-MAY-2002 (first entry)

XX Arabidopsis NADPH dependent thioredoxin reductase DNA (NTR).

XX Transgenic plant; thioredoxin reductase; starch; protein; grain;
 KW milling process; enzyme; ds.

XX Arabidopsis sp.

XX Key Location/Qualifiers
 FH CDS 10..1011

FT CDS /*tag= a

FT CDS /product= "Arabidopsis NTR"

XX W0200198509-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-EP006918.

XX 21-JUN-2000; 2000US-00598747.

XX (SYN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Desai NM, Gasdaska PY;

XX NPI; 2002-179557/23.

XX P-PSDB; AAE18732.

XX Transgenic plant coding for eukaryotic thioredoxin reductase at elevated
 PT levels useful for separating the starch and protein components of grain
 PT in a milling process.

XX Claim 12; Page 79; 86pp; English.

XX The present invention relates to a transgenic plant comprising
 CC heterologous DNA coding for eukaryotic thioredoxin reductase integrated
 CC into its nuclear or plastid genome and use of thioredoxin reductase for
 CC separating the starch and protein components of grain in a milling
 CC process. Transgenic plant is used for separating the starch and protein
 CC components of grain in a milling process. Transgenic plant may be used to
 CC produce thioredoxin reductase at elevated levels. Delivery of thioredoxin
 CC reductase eliminates the need to develop exogenous sources for addition
 CC during processing. Secondly, physical disruption of seed integrity is not
 CC necessary to bring the enzyme in contact with the storage or matrix
 CC proteins of the seed prior to processing or as an extra processing step.
 CC The present sequence is Arabidopsis NADPH dependent thioredoxin reductase
 CC DNA (NTR)

XX Sequence 1021 BP; 178 A; 385 C; 304 G; 154 T; 0 U; 0 Other;

Query Match 42.1%; Score 562.8; DB 6; Length 1021;

Best Local Similarity 74.2%; Pred. No. 1.9e-118;

Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;

QY 113 CGTCCGACGCGATCTGATCATCGGAGCGGTCCCGCTCGGACACAGGCGCATCT 172

DB 26 CTCACAACACCCGCTCTGATGTTGGCTCCGGCCGCTGCCCCACACCCGCGCATCT 85

RESULT 6

AAC43307

ID AAC43307 standard; DNA; 1152 BP.

XX AAC43307;

XX

DT 17-OCT-2000 (first entry)

QY 173 ACGCGGCGCGCGGAGCTCAAGCCTGTGCTCTTTCGAGGGCTGGATGCCCAAGACATCG 232
 DB 86 ACGCGGCGCGCGGAGCTGAAGCGCTCTCTTTCGAGGGCTGGATGCCCAAGACATCG 145
 QY 233 CCGCGGCGCGGAGCTCAACACCAACCAAGCTGCGAGAACTTCCCGGGCTTCCCAACG 292
 DB 146 CCGCGGCGCGGAGCTCAACACCAACCAAGCTGCGAGAACTTCCCGGGCTTCCCGGAG 205
 QY 293 GCATCATGCGCGCGGAGCTCATGAGCAACTGCGCGGCGGAGTCCCTGCGCTTTGGCACCA 352
 DB 206 GCATCCTCGCGCTGAGCTGACCGCAAGTTCCGAGCAGAGGAGCGCTTGGCACCA 265
 QY 353 ACATCCTCTCGAGAGCGCTGACCGCGCTGCACTTTTGGGCTGCCCATTTCCGAGTTAGTG 412
 DB 266 CCATCTTCAACGAGACCGTGAACAAAGTGGACTTCTCGACCAAGCGCTTCAAGCTTTCA 325
 QY 413 CAGACTCACAAACCGTCTCGCGGATGCGGTATATGTTGCCACGCGGAGCGCTGCGCGGC 472
 DB 326 CCGACTCAAGGCGCATCTCGCGGAGCGCGGTGATCTCGCCATCGCGCGCTGCGCGAGT 385
 QY 473 GCCTCCACTTCCCGGCTC-----CGATGCACTGGAACCGCGGCTATCCG 520
 DB 386 GGCTCTCTCTTGTGGGCTCCGGGAGGTGCTCGCGGCTCTTGGAAACCGCGGATCTCCG 445
 QY 521 CTTGTGCGCTGTGTGACGCTGCGCGGCTCTTTCGTTAAAGCCCATCGCGCTCATAG 580
 DB 446 CTTGCGCTGTGTGCGAGCGCGCGCGCGGATCTTCCGCAACAGCGCTGCGCTGTATCG 505
 QY 581 CGCGCGGAGTCTCGCTATGAGGAGTGCATTTCTTCCACCAAGTACGGTCCCAAGTCT 640
 DB 506 GTGGCGGAGACAGCGCGATGAGGAGGCGCAACTTCTTCCAAAGTACGGTCCCAAGTGT 565
 QY 641 ACATCATCCACCGCGCAATACCTTCCGTGCTTCCAAAGTATCATGACGCGCGCGCTTG 700
 DB 566 ACATCATCGACCGCGCGGACGCTTCCGCGCTTCCAAAGTATCATGACGCGCGCGCTCT 625
 QY 701 AGAACCCCAAAATTAAGTCTCTGAGACTCGGAGTGTGTGAGGCTATGCGCGCGCAA 760
 DB 626 CCAACCCCAAAATTAAGTCTCTGAGACTCTGAGTGTGTGAGGCTATGCGCGCGCAA 685
 QY 761 ACGCGCGCGCTTGGCTGAGTAAAGTTAAGAACTTCTGATGTGAGGCTTCCGATC 820
 DB 686 AGCGCGAGCTGTCTCGCGGCTCAAGGTGAGAACTGCTGACCGCGAGCTGTCCGACC 745
 QY 821 TTGAGTGTGTGCGCTTCTTTCGCGATGCGCGGATGAGCGCGGAGCAAAATTCCTGGGG 880
 DB 746 TCAAGGTGTCCGCTCTTCTTCCGATCGCGCGGATGAGCGCGGAGCAAAATTCCTGGAG 805
 QY 881 GACAGCTTGAATCGATTGAGTGTGAGAACTTCTGATGTGAGGCTTCCACTCACCA 940
 DB 806 GCGCGCTGAGCTGGACTCCGAGGCTACTGTTGACCAAGCGCGGACCAACCGAGCT 865
 QY 941 GTGTAAAGGTGTATTGCTGCTGCGGAGCTGCGAGCAAGAGTACCTCAGGCGATTA 1000
 DB 866 CCGTGTGCGCTGTTTTCGCGCGCGGCGGCTGCGAGCAAGAGTACCGCGGAGGCGATCA 925
 QY 1001 CTGCGCTGATCAGGCTGATGCTGCTTGGAGCTGAGCTGAGCACTACCTGCGAGGATCG 1060
 DB 926 CCGCGCGCGGACCGCTGATGCGCGCTGAGCGCGGCTGAGCGCGGAGGATCG 985
 QY 1061 GTGCACAGGCGGAAAGTCTGATT 1084
 DB 986 GTTCCAGAGGCGAAAGTCCGACT 1009

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38790.
XX DE Hybridisation assay; Genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW Promoter; termination sequence; 5S.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.
XX PR 09-MAR-1999; 99US-0123548P.
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XX PR 29-MAR-1999; 99US-0126785P.
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XX PR 27-AUG-1999; 99US-0151065P.
XX PR 27-AUG-1999; 99US-0151066P.

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PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
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PR 26-OCT-1999; 99US-0161360P.
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PR 28-OCT-1999; 99US-0161820P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 34.2%; Score 457; DB 3; Length 1152;
Best Local Similarity 67.9%; Pred. No. 2, Se-94;
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

Qy 128 TCTGCTATCTGGAGCGGTTCGCTGCGCACACGCGACCCATCTACGCGGCCCGCGCG 187
Db 182 TTTGCTATCTGCGAGTGGACACGACGACGCGCGCGATCTATGCTACGAGCGCG 241

Qy 188 AGCTCAAGCTGCTCTTCGAGGCTGATGTCACACGACATCGCGCGCGGCGAGC 247
Db 242 AGCTTAAGCTCTCTCTTCGAGGATGATGCTACGACATCGCTCCGCGCGGTCAAT 301

Qy 248 TCACCAACCAACCGACGCTGAGAACTTCGCGGCTTCCCAACGCGCATCTACGCGCGC 307
Db 302 TAACTACCAACCAACCGACGCTGAGAACTTCCTCGGTTCCCTGAGGTATCTCGGTAT 361

Qy 308 ACCTCATGACACTCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367
Db 362 ATATCGTTGAGAAATTCAGAAACAAATCGAGAGATTTGGAATTCAGATCTTCAGGAA 421

Qy 368 CCGTCAACCGCGCTGACTTTTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 427
Db 422 CTGTTAACCAAGTTGATTTCTCAACGAAACCGTTTAAAGCTATTCTACTGATTCGAGAACTG 481

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RESULT 7
ABZ14681
ID ABZ14681 standard; DNA; 1152 BP.

XX ABZ14681;

XX 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2486.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026695.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

XX 22-JUN-2001; 2001US-0300111P.

Qy 428 TCTCGCGATGCGGTATCTGTCGCAACGCGAGCGCTCGCGCGCGCTCCACTTCGCCG 487
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 Qy 488 GGTCCGATGCA-----TACTGGAACCGCGCATCTCCGCTGTGCGCGTGTG 535
 Db 542 GATCTGGTGAAGGTAATGTTGGTATTTTGGATCTGTTGATCTCCGCTGTGCTGTTGGC 601
 Qy 536 ACGGTGCGCGCCCATCTTCGTTAAACCAAGCCATCGCCGTCATAGGCGCGCGGACCTCG 595
 Db 602 ACGGAGCTGCTCCGATTTTGGATTAAGCTCTTGGGTATTTGGTGTGTTGATTCAG 661
 Qy 596 CTATGGAAGAGTCCAAATTCCTCAACCAAGTACGCTCCACGCTACATCAATCAACCGCC 655
 Db 662 CTATGGAAGAGTCCAAATTTCTGACTAAGTATGATCTAAGGTTTATATTATTCATAGGA 721
 Qy 656 GCAATACCTTCGCTGCTTCCAAAGATCATGCAAGCCAGCGCTTGGAGAACCCCAAAATTA 715
 Db 722 GGGATACGTTTGGGCGCTCTAAGATTTAGCAGCAGAGCTTTGTCTTAACCTTAAGATTG 781
 Qy 716 AGTCTCTGGAATCTCGGAAGTTGTGAGGCTTAATGGCGCGCAACGCGCGGCCCATTTGG 775
 Db 782 AAGTGAATTTGGAATCTCTGCGCTGCTTGGGCGCTATGCTGATGAAATGCACTGTTCTTG 841
 Qy 776 CTGCGCTAAAGGTTAAGAACTTCTGATGCTGAGGTCTCGGATCTTTCAGTGTCTGCGCC 835
 Db 842 GAGGATTTGAGGTCAGAAATGTTGTTACTGCGGATGTTTCAGATCTGAAGTGTCTGGAT 901
 Qy 836 TCTTCTTCGCAATCGGCAATGAGCGCGCACCAAAATTCCTGGCGCGGACAGCTTGAATCG 895
 Db 902 TGTCTTTCGCTATGCTCATGAGCAGCTACGAAGTTTTTGGATGCGGCGCTTGGAGCTTG 961
 Qy 896 ATTCAAGATGTTATGTCGAACCAAGCCAGGTTCCACTCACACAGTGTAAAGGTTGAT 955
 Db 962 ATGAAGATGTTATGTTGTGACCAAGCCAGGCTACTAAGACGAGCTGCTGTTGTTGAT 1021
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 Qy 1076 AGTCTGATTCA 1086
 Db 1142 AGAGTCAATTCA 1152

XX (Scrip) RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Xreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
XX
XX Claim 14; SEQ ID NO 2486; 577pp + Sequence Listing; English.
XX
XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
XX Sequence 1152 BP; 281 A; 222 C; 308 G; 341 T; 0 U; 0 Other;
Query Match 34.2%; Score 457; DB 6; Length 1152;
Best Local Similarity 67.9%; Pred. No. 2.5e-94;
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;
128 TCTGCTATCGGAGCGGTCCCGCTGGCGACGAGCCATCTACGCGCGCGCGCG 187
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248 TCACACACACCGAGCTCGAGAACTTCGCGGCTTCCCAACGAGATCGTGGCGCGCG 307
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308 ACCTCATGAGCACTCGCGCGCGAGCTCCCTGCGCTTGGCGACCAACATCTCTCCGAGA 367
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368 CCGTCACCGCGCTGACTTTTCGGCTCGCCATTCGAGATTAGTGCAGACTCCACACCG 427
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536 AGGTGCGCGCCCATCTTCGTTACAGACCCATCGCGCTCATAGCGCGCGCGACTCG 595
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596 CTATGAGGAGTCCCAATTTCTCCAAAGTACGGCTCCCACTGATCATATCCACGCC 655
662 CTATGAGGAGGAGTATTTCTGATCTAGTATGATCTAAAGTTTATATTATTCATAGA 721
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Qy 1076 AGTCTGATTGA 1086
Db 1142 AGAGTGATTGA 1152
RESULT 8
ADA67905 standard; DNA; 1152 BP.
XX ID
XX ADA67905;
AC
XX 20-NOV-2003 (first entry)
DT
XX Arabidopsis thaliana gene, SEQ ID 148.
DE
XX Plant; bacterial infection; fungal infection; viral infection; ds.
KW
XX Arabidopsis thaliana.
OS
XX Arabidopsis thaliana.
XX
XX W02003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 148; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to

PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
PR	18-JUN-1999;	99US-0139457P.
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PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	22-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	25-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
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PR	25-OCT-1999;	99US-0161406P.
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PR	28-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
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PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match 34.2%; Score 457; DB 3; Length 1375;
Best Local Similarity 67.9%; Freq. No. 2.6e-94; Mismatches 300; Indels 12; Gaps 1;
Matches 659; Conservative 0;

Qy	128	TCTGTCATCATCGGAGCGGTCCCGCTGGCCACACGGGAGCCATCTACGGGCGCGCGCGG	187
Db	171	TTTGTCATGCTCGGAAGTGGACACACACGGGCGGATCTATGTCATCGAGAGCGG	230
Qy	188	AGCTCAAGCTTGCTTTCGAGGGTGGATGGCCACACATCGCGGGGCGGCGAGC	247
Db	231	AGCTTAAGCCTTCTTCTTCGAGGATGGATGGCTAACGACATCGTCCCGCGGCTCAAT	290

QY 248 TCACCACACACCGACGTCGAGAACTTCCCGGGCTTCCCAACGGCAATCAGGCGCG 307
Db 291 TAACTACAAACACCGACGTCGAGAACTTCCCGGGCTTCCCAACGGCAATCAGGCGCG 350
QY 308 ACCTCATGGAACAATGCGCGCGGCACTTCCCGGGCTTCCCAACGGCAATCAGGCGCG 367
Db 351 ATATCGTTGAGAAATTCAGAAACAAATCGGAGAGATTTGGAACTACGATCTTCACGAAA 410
QY 368 CCGTCACCGCGGTCGACCTTTTCGGCGCTGCCCAATCCGAGTTAGTGCAGACTCCCAACCG 427
Db 411 CTGTAAACAAGTTGATTTCTCATCGAAACCGTTTAAAGCTATTCACGANTCGAGAACTG 470
QY 428 TCCTCGCGAGCGGTTATCGTTGCCACGAGGCGGTCGCGGGCGGCTCCACTTCCCG 487
Db 471 TTCTCGCGGATCTGTAATCATTTCTACTGAGAGCTGTGCTAAAGCTCTTACGTTCACTG 530
QY 488 GGTCCGATGCA-----TACTGGAACCGCGGCACTCTCCCGCTGTGCGCTGCTGTG 535
Db 531 GATCTGTTGAGGTAATGTTGTTTGGAACTCGTGTATCTCCGCTTGTGCTGTTTGG 590
QY 536 ACGTGGCGGCGGCTTCTCCGTAACAGCCGATCGCGTCTATAGCGCGGCGGCTCCG 595
Db 591 ACGGAGCTGCTCCGATTTTATAGAAATAAGCTCTTGTGTTTATGTTGTTGTTGTTGAT 650
QY 596 CTATGAGGAGTCCAAATTTCTCCACAGTACGGCTCCCAAGCTTACATCATCCACGCG 655
Db 651 CTATGAGGAGTCCAAATTTCTCCACAGTACGGCTCCCAAGCTTACATCATCCACGCG 710
QY 656 GCAATACCTTCCGCTTCCAGATCATGACGCGGCGGCTTCCAGAACCCCAAAATA 715
Db 711 GCGATACGTTTGGGCGCTTAAGATTTATGACGAGAGAGCTTTGTCTAACCCCTAAGATTG 770
QY 716 AGTCTCTGCGGACTCGGAATGTCGAGGCTATGCGGCGGCGGCGGCGGCGGCGGCGG 775
Db 771 AAGTGATTTGGAACTCTCGCGGCTTGGCGGCTATGCGGCGGCGGCGGCGGCGGCGG 830
QY 776 CTGCGGCTAAAGTTAAGAACTTACTGAGTGTGAGGCTCTCGGATCTTCAAGTGTCTG 835
Db 831 GAGGATTGAAGTGAAGATGTTGTTACTGCGGATGTTTCAGATCTGAAGGTTCTGGAT 890
QY 836 TCTTCTCCGCTGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 895
Db 891 TGTCTCTGCTATGCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 950
QY 896 ATTACATGCTTATGCGGAAACCAAGCGGCTTCCACTCAGGAGTGTAAAGGCTGTAT 955
Db 951 ATGAAGATGTTATGTTGACCAAGCGGCTTACTTAAAGCGGCTGTGTTGTTGAT 1010
QY 956 TTGCTGCTGCGGAGTGCAGGAGCAAGATACCGTCAAGGCGGCTTACTGCGGCTGATCAG 1015
Db 1011 TTGCTGCTGCGGAGTGTTCAGACAGAGATATAGACAGGCGGCTTACTGCTGAGGAACTG 1070
QY 1016 GGTGATGCTGCTGATGAGGCTGAGCACTACTGCGAGGAGATCGTGCACAGGAGGAA 1075
Db 1071 GGTGATGCTGCTGATGAGGCTGAGCACTACTGCGAGGAGATCGTGCACAGGAGGAA 1130
QY 1076 AGTCTGATGA 1086
Db 1131 AGATGATGA 1141

RESULT 10
ID AAL54488
XX AAL54488 standard; DNA; 6357 BP.
XX AC AAL54488;
XX DT 10-APR-2003 {first entry}
XX Thioresoxin reductase variant DNA sequence #10.
XX DE
XX Ophthalmological; virucide; vulnerary; vasotropic; antiallergic;
KW cofactor specificity; thioresoxin reductase; TR; non-allergenic food;

KW computational mutagenesis; scaffold protein; oil body; animal feed;
KW digestibility; gluten; protein disulfide isomerase; PDI; enzyme;
KW scleroprotein; gelled; food; nitrosative stress response; eye disease;
KW cataract; oxidative stress; ischemic-reperfusion; acute lung injury; ds.
XX Unidentified.
XX WO200290300-A2.
XX 14-NOV-2002.
XX 06-MAY-2002; 2002WO-US014358.
XX 04-MAY-2001; 2001US-0289029P.
XX 05-APR-2002; 2002US-0370609P.
XX 29-APR-2002; 2002US-00370609.
XX (XENC-) XENCOR.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;
XX Luginbuhl P, Muchhal U;
XX WPI; 2003-111951/10.
XX Altering cofactor specificity of target protein, e.g. thioresoxin
XX reductase useful for reducing antigenicity of glutens in wheat, barley,
XX or treating disulfide linkages present in proteins, by computational
XX mutagenesis.
XX Disclosure; Fig 16; 212pp; English.
XX The invention relates to a novel method for altering the cofactor
XX specificity of a target protein (e.g. thioresoxin reductase (TR)) by
XX computational mutagenesis. This method involves inputting a set of
XX coordinates for a scaffold protein comprising amino acid positions,
XX applying at least one protein design cycle; and generating a set of
XX candidate variant proteins with altered cofactor specificity. The novel
XX method is useful for altering the cofactor specificity of TR scaffold
XX proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium
XX leprae, Saccharomyces, Neurospora crassa, Arabidopsis, and human. Another
XX method of the invention is useful for making oil bodies which are useful
XX in the preparation of non-allergenic foods or in the preparation of
XX animal feeds to improve the digestibility of the feeds. The variant TR
XX protein is useful for reducing the antigenicity of glutens in wheat, rye
XX or barley, to reduce alternative substrates for thioresoxin reductases,
XX including a number of plant and mammalian proteins found to contain
XX thioresoxin domains e.g. protein disulfide isomerase (PDI). The variant
XX TR protein is useful as a redox partner in compositions used for treating
XX disulfide linkages present in proteins such as enzymes, e.g., proteases,
XX amylases, etc; and structural proteins such as scleroproteins.
XX Compositions comprising variant TR proteins and PDI are useful for
XX generating protein disulfide crosslinks yielding high molecular weight or
XX gelled compositions, and thus is useful in food processing. A further
XX method of the invention is useful for producing plants expressing variant
XX TR protein, e.g., corn and soybean provides grains with altered storage
XX protein quality as well as grains that perform qualitatively differently
XX from normal grain during industrial processing or animal digestion of
XX variant TR proteins in combination with thioresoxin, which can be used to
XX manipulate nitrosative stress, to upregulate nitrosative stress
XX responses, and thus is useful for treating eye diseases, such as
XX cataracts, where it inhibits or reverse formation of cataract in eye. The
XX variant TR protein in combination with thioresoxin is also useful for
XX minimizing oxidative stress and ischemic-reperfusion induced in acute
XX lung injury. This polynucleotide sequence represents a thioresoxin
XX reductase variant DNA sequence of the invention
XX Sequence 6357 BP; 1518 A; 1643 C; 1654 G; 1542 T; 0 U; 0 Other;

Query Match 33.0%; Score 440.6; DB 7; Length 6357;
Best Local Similarity 66.2%; Pred: No. 2.1e-90;
Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;

QY	408	TAGTGCAGACTCCACAAACGCTCTCGCCGATGCGGTATCGTTGCCACGGAGCGCTCGC	467
Db	5645	ATTACAGATTCACAGGCAATCTCGCTGACGCTGTGATCTCGCTACTGAGCTGTGGC	5704
QY	468	GGGGCCCTCCACATTCGCCGGTCCGATGCA-----TACTGGAACCGCGGAT	515
Db	5705	TAAAGCGCTTAGCTTCGTTGGATCTGGTGAAGTTCTGGAGTTCTGGAGTTCTGGNAACCGTGAAT	5764
QY	516	CTCGCCTGTGCGCTCTGTGAGGTCGCGCCCATCTTCGTAAACAAGCCCATCGCCGT	575
Db	5765	CTCCGCATGCGCTGTTGGACGGAGCTGCTCGATATTCCGTACAAACCTCTTGGCGT	5824
QY	576	CATAGCGCGCGGACTCGCTATGAGAGAGTCCAAATTCCTCCAAAGTACGGCTCCCA	635
Db	5825	GATCGGTGGAGCGGATTCAGCAATGGAAGAACAAACTTCTTACAAATATGATCCAA	5884
QY	636	CGTCTACATCAACACCGCGCAATACCTTCGTCCTCCAGATCATCGAGGCCAGGCG	695
Db	5885	AGTGTATATAATCCATCGCTACGATGCTTTAATCGCTTAGATATGCAAGCGCGC	5944
QY	696	GCTTGAGAACCCCAAAATTAAAGTCTCTGGGACTCGGAAGTTGTCGAGGCTATGGCGG	755
Db	5945	TTTGTCTAATCTAAGATTGATGTGATTTGGAACCTGCTGTTGTGGAAGCTTATGGAGA	6004
QY	756	CCCAACGGCGGCCCATTTGGCTGGCGTAAAGTTAAGAACCTACTGAAATGGTGGTCTC	815
Db	6005	TGGAGAAAGAGATGCTCTTGGAGGATTGAAGTGAAGAAATGGGTTACCGGTGATGTTT	6064
QY	816	GGATCTTCAGGTGTCTGGGCTCTTCTTGGCCATCGGGCATGAGCGCGGACCCAAATTCCT	875
Db	6065	TGATTTAAAGTTTCTGGATTGTTCTTTGCTATTGTTGATGAGCCAGCTACCAAGTTTT	6124
QY	876	GGCGGACAGCTTGAACCTCGATTCAAGTGTATGTGGAACCAAGCCAGGTTCCACTCA	935
Db	6125	GGATGGTGTGTGAGTTAGATTGGATGGTTATGTGTACGNAAGCCCTGGTACTACACA	6184
QY	936	CACCAAGTGTAAAGGTGTATTTGCTGCGGACGTGAGGACAAGAAGTACCGTCAGGC	995
Db	6185	GACTAGCGTTCGGAGTTTTCGCTGCGGTCATGTTCAAGATAGAGATAGGCAAGC	6244
QY	996	CATTACTCGCGTGGATCAGGTGCAATGGCTGCATTTGACGCTGAGCACTACCTCCAGGA	1055
Db	6245	CATCACTGCTGCAGGAACCTGGGTGCATGGCAGCTTTGGATGCAGAGCATTACTTACAAGA	6304
QY	1056	GATCGGTGCACAGGAGGGAAGTCTGATTGACT	1088
Db	6305	GATTGATCTCAGCAAGGTAGAGTGNATTGACT	6337

;; PRIOR FILING DATE: 2002-04-29
;; PRIOR APPLICATION NUMBER: US 10/141,531
;; PRIOR FILING DATE: 2002-05-06
;; PRIOR APPLICATION NUMBER: US 60/289,029
;; PRIOR FILING DATE: 2001-05-04
;; NUMBER OF SEQ ID NOS: 239
;; SOFTWARE: Patentin version 3.2
;; SEQ ID NO 43
;; LENGTH: 6357
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE: Artificial sequence
;; OTHER INFORMATION: synthetic
US-10-290-072-43

Query Match 32.6%; Score 435.8; DB 13; Length 6357;

Best Local Similarity 65.9%; Pred. No. 3.2e-125;
Matches 654; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

QY	108	CGCTCCGCTCGGACGCGCATCTGTCATCATCGGAGGGTCCGCTGGCACAGGCGAGC	167
DB	5345	CGAACTCAACAACAAAGGCTCTGTATCGTAGGAAGTGGCCAGCGCACACAGCGCGC	5404
QY	168	CATCTAGCGGCGCGCGGAGCTCAAGCCGTGCTCTTCGAGGGCTGGATGGCAACGA	227
DB	5405	GAITTAGCGAGTAGGCTGAATTAACCTCTCTCTCGAAGGATGGATGGCTAACGA	5464
QY	228	CATCGCGGCGGCGCGGAGCTCAACACACCGAGCTGAGAACTTCGCGGCTTCCC	287
DB	5465	CATCGCTCCGCGTGGTCACTAACACACCGAGCTGAGAACTTCGCGGATTTCC	5524
QY	288	CAACGCGCATCATGGCGCGCGAGCTCAACCGAGCTGAGAACTTCGCGGCTTCCC	347
DB	5525	AGAAGGTATTCGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCAATTCG	5584
QY	348	CACCAACATCTCTCGAGACCGCTCAACCGCGCTGAGAACTTCGCGGCTTCCC	407
DB	5585	TACTAOCATATTTACAGACGCTGACGAAAGTCCATTTCTTCGAAACCGTTTAA	5644
QY	408	TAGTGCAGACTCCACACCGCTCTCGCGGATCGGTTATCGTTCGCGGCGCGTGC	467
DB	5645	ATTCACAGATTCGAAGGCGATTCGCTGAGCTGTGATTCGCTACTGAGCTGTGC	5704
QY	468	CGCGCGCTCCACATTCCTCCGCGGCTCGATGCA-----TACTGGAAACCGCGCAT	515
DB	5705	TAGCGGCTTAGCTTGTTGATCTGGTGAAGTCTCGAGGTTCTCGAAACCGTGAAT	5764
QY	516	CTCGGCTTGCCTGTGTAGCGTGGCGCCCATCTTCGTTAAGCAAGCCATCGCGT	575
DB	5765	CTCGGCTTGCCTGTGTAGCGTGGCGCCCATCTTCGTTAAGCAAGCCATCTTCG	5824
QY	576	CATAGGCGGCGGACTCCGCTATGGAGAGTCCAAATTCCTCACCAAGTACGGCTCCCA	635
DB	5825	GATGGTGGAGGCGATTCAAGCAATGGAGAGCAAACTTTCTTACAAAATATGATCCAA	5884
QY	636	CGTCTACATCATCAACCGCGCAATACCTTCGCTGCTTCCAGATCATCGAGCCAGGC	695
DB	5885	AGTGTATATATATCCATCGTACGATGCTTTAATGCGCTTAAGATATGACGAGCGGC	5944
QY	696	CTTTGAGAACCCCAAAATTAAGTCTCTCGGACTCGGAAGTGTTCGAGGCTATGGCG	755
DB	5945	TTTGTCTATCTAAGATTGATGATTTGAACTCTGCTGTGTGAGAGTTATGAGA	6004
QY	756	CGCAACCGCGCGCCATATGGCTGGGTAAGGTTAAGAACTTCTGATGTGAGGTTCT	815
DB	6005	TGGAGAAAGATGTGCTTCGAGGATTCGAAAGTGAAGAAATGTTTACCGGTGATTTT	6064
QY	816	GGATCTTCAGGTGTCTGCGCTCTTCGCGCATCGGCGATGAGCGCGGACCAATCTCT	875
DB	6065	TGATTTAAAGTTTCTGATGTTCTTTCGCTATTTGCTATTTGCTCATGAGCGAGTTC	6124
QY	876	GGGCGGACAGCTTGAATTCAGATGTTTATGTGGAAACCAAGCCAGGTTCCACTCA	935

DB	6125	GGATGCTGCTGTGAGTTAGATTCCGATGCTTATGTTGTCAAGAGCTGGTACTACACA	6184
QY	936	CACCACTGTAAAGGCTGTATTTTCTCTGCGCAGCGTGCAGGACAAAGTACCGTCA	995
DB	6185	GACTAGCGTTCCCGGAGTTTTCGCTGCGGCTGATGTTCAAGGATAGAGTATAGGCA	6244
QY	996	CATTACTGCGCTGCGATCAGGCTGATGGCTGATTTGGACGCTGACACTACCTGCA	1055
DB	6245	CATCACTGCTGCGAGAACTGGGTGATGGCACTTTTGGATGCAAGCATTTACTTACA	6304
QY	1056	GATCGGCTGCACAGGAGGGAAGTCTGATTGACT	1088
DB	6305	GAITGGATCTCAGCAAGGTAAGAGTGATTGAGT	6337

RESULT 15

US-10-290-072-45

Sequence 45, Application US/102900072

Publication No. US20030211511A1

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.

APPLICANT: Daimia, Bipin K.

APPLICANT: Desjarlais, John R.

APPLICANT: Heifetz, Peter

APPLICANT: Luginbuhl, Peter

APPLICANT: Muchhal, Umesh

TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity

FILE REFERENCE: A-71457-3

CURRENT APPLICATION NUMBER: US/10/290,072

CURRENT FILING DATE: 2002-11-06

PRIOR APPLICATION NUMBER: US 60/370,609

PRIOR FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: US 60/376,682

PRIOR FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: US 10/141,531

PRIOR FILING DATE: 2002-05-06

PRIOR APPLICATION NUMBER: US 60/289,029

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 239

SOFTWARE: Patentin version 3.2

SEQ ID NO 45

LENGTH: 6357

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: synthetic

US-10-290-072-45

Query Match 32.6%; Score 435.8; DB 13; Length 6357;

Best Local Similarity 65.9%; Pred. No. 3.2e-125; Indels 12; Gaps 1;

Matches 654; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

QY	108	CGCTCCGCTCGGACGCGCATCTGTCATCATCGGAGGGTCCGCTGGCACAGGCGAGC	167
DB	5345	CGAACTCAACAACAAAGGCTCTGTATCGTAGGAAGTGGCCAGCGCACACAGCGCGC	5404
QY	168	CATCTAGCGGCGCGCGGAGCTCAAGCTGTGCTTCTTCGAGGGCTGGATGGCAACGA	227
DB	5405	GAITTAGCGAGTAGGCTGAATTAACCTCTCTCTCGAAGGATGGATGGCTAACGA	5464
QY	228	CATCGCGGCGGCGCGGAGCTCAACCGAGCTGAGAACTTCGCGGCTTCCC	287
DB	5465	CATCGCTCCGCGTGGTCACTAACACACCGAGCTGAGAACTTCGCGGATTTCC	5524
QY	288	CAACGCGCATCATGGCGCGCGAGCTCAACCGAGCTGAGAACTTCGCGGCTTCCC	347
DB	5525	AGAAGGTATTCGAGTAGAGCTCACTGACAAATTCGTAACATCGGAGCAATTCG	5584
QY	348	CACCAACATCTCTCGAGACCGCTCAACCGCGCTGAGAACTTCGCGGCTTCCC	407
DB	5585	TACTAOCATATTTACAGACGCTGACGAAAGTTCCTTCTTGAACCGTTTAACT	5644

QY 756 CGCAAAACGGCCGCAATGGCTGGCTAAAGTTAAGAACCTACTGAATGTGAGTCTC 815
Db 6005 TGGAGAAAGAGATGTGCTTGGAGGATTGAAGTGAAGATGTGTTACCGGTGATGTTT 6064
QY 816 GGATCTTCAGGTGCTGCGCTCTCTTCGCCATCGGCGATGAGCGGCGACCAAAATTCCT 875
Db 6065 TGAATTTAAAGTTCTGATGTTCTTCTGCTATGCTATGCTGATGAGCGAGTACCAAGTTT 6124
QY 876 GGGCGGACAGCTTGAACCTGATTCAGATGGTATGTGAAACCAAGCCAGGTTCACATCA 935
Db 6125 GGATGGTGTGATGATTTGCTGCGAGTTCGATGTTGCTGCGAAGCTTGTACTACACA 6184
QY 936 CACCAAGTAAAGGTGATTTGCTGCGAGTTCGAGCTGAGCAAGAGTAGTACCGTCAGGC 995
Db 6185 GACTAGCGCTCCGAGTTCCTGCTGCGGATGATGTTGAGTAAAGATGATGAGCAAGC 6244
QY 996 CATTAAGTGGAGTGGATGCTGCGAGTTCGAGCTGAGCAAGAGTAGTACCGTCAGGC 1055
Db 6245 CATCACTGCTGAGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 6304
QY 1056 GATCGGTGACAGGAGGAAAGTCTGATGACT 1088
Db 6305 GATTGGATCTCAGCAAGGTAAGAGTGTGAGT 6337

RESULT 13

US-10-141-531-38
; Sequence 38, Application US/10141531
; Publication No. US20030100743A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-2/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/10/141,531
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/289,029
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 6357
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-141-531-38

Query Match 33.0%; Score 440.6; DB 15; Length 6357;
Best Local Similarity 66.2%; Pred. No. 9.9e-127;
Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;
QY 108 CGTCCGCTCCGCAACGGGATCTGATGATGATGATGATGATGATGATGATGATGATGAT 167
Db 5345 CGAAACTCACAACACAGGCTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 5404
QY 168 CATCTAGCGGCGCGCGGAGTCAAGCTGCTCTTCGAGGCTGATGATGATGATGATGATGATGAT 227
Db 5405 GATTACGAGTATGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5464
QY 228 CATCGCGCGGCGGCGGAGTCAACACACAGGCTGATGATGATGATGATGATGATGATGATGATGAT 287
Db 5465 CATCGCTCCCGGTGGTCAACTAAACACACAGGCTGATGATGATGATGATGATGATGATGATGATGAT 5524
QY 288 CAAGGATCATGGCGCGCGAGTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 347
Db 5525 AGAAGGATCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5584

QY 348 CACCAACATCTCTCCGAGACCGTCAACCGCGCTCGACTTTTTCGGCTGCCCCATTCGAGT 407
Db 5585 TACTACGATATTACAGAGACGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 5644
QY 408 TAGTGAGAGCTCACAACCGTCTCGCGAGTGGGTATGTTGCTGCGACGGAGCGGTGCG 467
Db 5645 ATTACAGATTTCAAGGCCATTCTCGCTGACGTGTGATTTCTCGCTACTCGAGCTGTGGC 5704
QY 468 GCGGCGCTCCACTTCCCGGGTCCGATGCA-----TACTGGAAACCGCGCAT 515
Db 5705 TAGCGGCTTAGCTTGTGGATCTGGTGAAGTTCGTGAGGTTTCTGGAAACCGTGAAT 5764
QY 516 CTCGCGCTGTGCGGTCTGTCAGGTCGCGCCCACTTCGCGTAAACAGGCCATCGCGCT 575
Db 5765 CTCGCGATGCGCTGTTTTCGACGAGCTGCTCGGATATTCGTAACAAACCTCTTGGCT 5824
QY 576 CATAGGCGGCGGAGCTCCGCTATGAGGAGTCCAAATTTCTCAACAGTACGCTCCCA 635
Db 5825 GATCGGTGAGGCGATTCAGCATGAGAGCAAACTTCTTACAAAATATGGATCAA 5884
QY 636 CGTCTACATCATCCACCGCGCAATACCTTCGCTTCCAAAGATCATGAGGCCAGGC 695
Db 5885 AGTGTATATATCATCCGCGCATGCTTTTTCGCTCTAAGATTATGAGCAGCGCGC 5944
QY 696 GCTTGAGAACCCCAAAATTAAGTCTCTGCGACTCGGAGTTCGTGAGGCTATGCGG 755
Db 5945 TTTCTTAATCTTAAGATTGATGATTTGGAATCTGCTGTTGTTGAGGCTATGAGA 6004
QY 756 CGCAACCGCGCGCCATTGGCTGCGCTGAAAGTTTAAAGCTTAAAGCTGTTGAGGCTCTC 815
Db 6005 TGGAGAAAGAGATGCTGCTGAGGATTTGAAGTGAAGATGTTGTTACCGTGTATGTTT 6064
QY 816 GGATCTTCAGGTGCTGCGCTCTCTTCGCCATCGGCGAGCGCGGACCAAAATTCCT 875
Db 6065 TGAATTTAAAGTTTCTGATGTTCTTTCGCTATGTTGCTGATGAGCTACCAAGTTT 6124
QY 876 GGGCGGACAGCTTGAACCTGATTCAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 935
Db 6125 GATGTT 6184
QY 936 CACCAAGTAAAGGTGATTTGCTGCGGAGTGGCGAGCTGCGAGCAAGAGTAGTACCGTCAGGC 995
Db 6185 GACTAGCGTTCGCGAGTTCGCTGCGGAGTTCGCTGCGGAGTTCGAGTAAAGATGATGAGCAAGC 6244
QY 996 CATTAAGTGGAGTGGATGCTGCGAGTTCGAGCTGAGCAAGAGTAGTACCGTCAGGC 1055
Db 6245 CATCACTGCTGAGGAGTGGGTCATGCGAGCTTGGATGCGAGCTTGGATGCGAGGATTAATTAACA 6304
QY 1056 GATCGGTGACAGGAGGAAAGTCTGATGACT 1088
Db 6305 GATTGGATCTCAGCAAGGTAAGAGTGTGAGT 6337

RESULT 14

US-10-290-072-43
; Sequence 43, Application US/10290072
; Publication No. US20030211511A1
; GENERAL INFORMATION:
; APPLICANT: Briggs, Steven P.
; APPLICANT: Dalmia, Bipin K.
; APPLICANT: del Val, Greg
; APPLICANT: Desjarlais, John R.
; APPLICANT: Heifetz, Peter
; APPLICANT: Luginbuhl, Peter
; APPLICANT: Muchhal, Umesh
; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
; FILE REFERENCE: A-71457-3
; CURRENT APPLICATION NUMBER: US/10/290,072
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US 60/370,609
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/376,682

Db 182 TTGTCATCGTCGAGTGGACGACGACACACACGCGCGGATCTATGATCGAGAGCGG 241
 Qy 188 AGCTCAAGCCTGTGCTCTTTCGAGGGCTGGATGGCCAAACGACATCGCCGCGCGGCGGACG 247
 Db 242 AGCTTAAGCCTCTCTCTTCGAGAGTGGATGGCTAAACGACATCGCTCCGCGCGGTCAT 301
 Qy 248 TCACCAACACACGACGTCGAGAACTTCCCGCGCTTCCCAACGCGATCATGGCGCGC 307
 Db 302 TAACTACACACGAGCTGGAACTTCCCTGGGTTCCCTGAGGTATTTCTCGGTATTG 361
 Qy 308 ACCTCATGACAACTGCGCGCGGCTGCTCTCTCTTGGCCAAACATCTCTCCGAGA 367
 Db 362 ATATCGTTGAGAAATTCAGAAACCAATCGAGAGATTTGGAACTACGATCTTCCGAGAA 421
 Qy 368 CGCTCACCGCGCTGCACTTTTCGGCTGCGCCATTCGAGTTAGTGCACACTCCACACCG 427
 Db 422 CNGTTAACAAAGTTGATTTCTCATGAAACCGTTTAAAGCTATTTCACTGATTCGAGACTG 481
 Qy 428 TCCTCGCGCATCGCGTTATGTTGTCACGAGAGCGCTGCGCGGCGCTCCACTTCCCG 487
 Db 482 TTCTCGCTGATTTCTGTAATCATTTCTACTGCGAGCTGTTGCTAAACGCTTCTAGCTTCACTG 541
 Qy 488 GGTCTCGATGCA-----TACTGGAACGCGGCACTCTCGCCCTGCGGCTGCTG 535
 Db 542 GATCTGGTGAAGTAATGGTGGTTTTGGATCGTGGTATCTCCGCTGGTGGTGTTCG 601
 Qy 536 AGCTGCGCGCCCTCTTCGTAACAAAGCCCATGCGCGCTCATAGGCGCGGCGACTCG 595
 Db 602 ACGAGCTGCTCCGATTTTAGAAATAAGCCCTCTTGTGGTTATTGGTGGTGGTGAATTCAG 661
 Qy 596 CTATGAGAGTCCAAATTTCTCACAAAGTACGCTCCACAGTCTACATCATCCACGCC 655
 Db 662 CTATGAGAGGACGCAATTTCTGATAGTATGATCTAAGTTTATTAATTCATAGGA 721
 Qy 656 GCAATACCTTCCTGCTTCCAAAGTATCATGACGCGCGGCGCTTGAGAAACCCAAATTA 715
 Db 722 GGGATACGTTTAGGCGCTTAAGATTTATGACGACGAGAGCTTTTGTCTAAACCTTANGATTG 781
 Qy 716 AGGTCTCTGCGACTCGGAAGTTGTGAGGCTATGCGCGCGCAAAACGCGCGCCATTGG 775
 Db 782 AAGTGAATTTGGACTCTGCGGCTGTGAGGCTATGAGTATGAAATGAGAGCTGTTCTTG 841
 Qy 776 CTGGCGTAAAGTTAAGAACCTATGAAATGTTGAGTCTCGATCTTCAAGTGTCTGCGC 835
 Db 842 GAGGATTGAAGGTGAAGAACTGTGTACTGGGGATGTTTTCAGATCTGAAGGTGTCTGGAT 901
 Qy 836 TCTTCTCGCATCGGCATGAGCGCGGACCAAAATTCCTCGCGGACAGCTTCAACTCG 895
 Db 902 TGTCTTTGCTATTGCTCATGAGCCAGTACGAGTTTGGATGGCGAGCTTGAAGCTTG 961
 Qy 896 ATTCAGATGGTTATGTGAACCAAGCCAGGTTCACTCAACCAAGTGTAAAGGTTAT 955
 Db 962 ATGAAGATGGTTATGTTGTCACCAAGCCAGGTACTACTAAGACGAGGTTGGTGTGTAT 1021
 Qy 956 TTGCTGCTGGGAGCTGACGAGCAGAGAGTACCGTCAAGGCCATTTACTGCGCTGGATCAG 1015
 Db 1022 TTGCTGCTGGAGATTTACAGACAGAGATATAGACGCGCTTCACTGCTGAGAACTG 1081
 Qy 1016 GGTGCATGGCTGCAATGGACCTGAGCACTACCTGCGAGGAGATCGGTGACAGAGGGA 1075
 Db 1082 GGTGCATGGCGCATTTGGATGACAGAGCACTTACTTACAGAGATTTGGATCTCAGGAGGTA 1141
 Qy 1076 AGTCTGATTGA 1086
 Db 1142 AAGTGAATTGA 1152

RESULT 12
 US-10-290-072-38
 ; Sequence 38, Application US/10290072
 ; Publication No. US20030211511A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Briggs, Steven P.

; APPLICANT: Dalmia, Bipin K.
 ; APPLICANT: del Val, Greg
 ; APPLICANT: Desjarlais, John R.
 ; APPLICANT: Heifetz, Peter
 ; APPLICANT: Luginbuhl, Peter
 ; APPLICANT: Muchhal, Umesh
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresoxin Reductase Activity
 ; FILE REFERENCE: A-71457-3
 ; CURRENT APPLICATION NUMBER: US/10/290,072
 ; CURRENT FILING DATE: 2002-11-06
 ; PRIOR APPLICATION NUMBER: US 60/370,609
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: US 60/376,682
 ; PRIOR FILING DATE: 2002-04-29
 ; PRIOR APPLICATION NUMBER: US 10/141,531
 ; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: US 60/289,029
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 239
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 38
 ; LENGTH: 6357
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-290-072-38

Query Match 33.0%; Score 440.6; DB 13; Length 6357;
 Best Local Similarity 66.2%; Pred. No. 9.9e-127;
 Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;
 Qy 108 CGCTCGCTCGCACGCGCATCTGTCATCATCGGAGCGTCCGCTCGCACACGCGAGC 167
 Db 5345 CGAACTCAACAACACGAGGCTCTGTATCTGTAGTAAGTGGCCAGCGGCACACACGCGGC 5404
 Qy 168 CATCTACGCGCGCGCGCGAGCTCAAGCTGTGTCTTCTGAGGCTCGATGGCCAAAGA 227
 Db 5405 GATTTACGCGAGCTAGGCTGAACCTTAAACCTCTCTCTCGAAGGATGGATGGCTAAAGA 5464
 Qy 228 CATCGCGCGCGCGCGAGCTCACACACACACGAGCTCGAGACTTCCCGGCTTCCC 287
 Db 5465 CATGCTCCCGTGGTCAACTAAACACACACGAGCTCGAGATTTCCCGGATTTCC 5524
 Qy 288 CAAAGCGCATCTGGCGCGCGACCTCATGGAACAATCGCGCGCGAGTCCCTCGCGCTTGG 347
 Db 5525 AGAAGGATTTCTCGAGTAGAGCTCACTGACAAATTCGTAAACAAATCGAGCGGATTCGG 5584
 Qy 348 CACCAACATCTCTCGAGACCGCTCACCGCGCTCGACTTTTTCGGCTCGCCATTCGGAGT 407
 Db 5585 TACTACGATATTACAGAGCGGTGACGAAAGTCGATTTCTTTCGAAACCGTTTAAAGCT 5644
 Qy 408 TAGTGCAGACTCCAAACCGCTCTCGCGATGCGGTATCGTTGCCAGGAGCGCTGCG 467
 Db 5645 ATTACAGATTCGAAGGCCATTTCTCGCTGACGCTGTGATTTCTGCTACTGAGGCTGCGC 5704
 Qy 468 GCGCGCTCTCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGCAT 515
 Db 5705 TAAGCGCTTAGCTTCTGTTGGATCTGGTGAAGGTTCTCGAGGTTTCTGGAACCGTGGAT 5764
 Qy 516 CTCCGCTGTGCGGTCTGTAGCGGTGCGCGCCCACTTTCGTAAACAGCCCATGCGCGT 575
 Db 5765 CTCCGCGATGCGCTTTCGACGAGCTGCTCCGATATTCGTAAACAAACCTCTTTCGCT 5824
 Qy 576 CATAGCGCGCGGACTCGCTATGAGGAGTCCCAATTTCTCCAGAGTCAAGTGGCTCCCA 635
 Db 5825 GATCGTGGAGCGGATTCAGCAATGGAAGAGCAAACTTTCTTCAAAATATGATTCNA 5884
 Qy 636 CGTCTACATATCCACCGCGCAATACCTTCCGCTTTCAGAGTATCATGAGGCGCAGGCG 695
 Db 5885 AGTGTATATATCATCGCGCGATGCTTTTCGTGCGTCTAAGATTTATGACGAGCGCGC 5944
 Qy 696 GCTTGAAGACCCCAAAATTAAGTCTCTCGGAGCTCGCAAGTGTGCGAGGCTATGCGG 755
 Db 5945 TTTGCTTAATCTTAAGATTGATTTGAACCTCTGCTCTGTTGGAAGCTTATGGAGA 6004

886	CTTGAATCGAATTCAGATGGTTATATGTAAGAAACCAAGCCAGGTTCTCACTCACACCAGTGA	945
QY		
887	CTTGAATTCAGATGGTTATATGTAAGAAACCAAGCCAGGTTCTCACTCACACCAGTGA	946
DB		
787	CTTGAATTCAGATGGTTATATGTAAGAAACCAAGCCAGGTTCTCACTCACACCAGTGA	846
DB		
946	AAGGGTGTATTTCCTGTCGCGACGTCAGAGCAAGAGTACCGTCAGGCCATTACTGCC	1005
QY		
847	GATGAGCTTTTTCGTCGTCGTGAATGTCAGAGTAAAGATATAGCAAGCTATTACAGCT	906
DB		
1006	GCTGGATCAGGGTGCATGGCTGCATTGGACGCTGAGCCTACTCTCAGAGAGATCGT	1062
QY		
907	GCTGGACCTGGGTATATGGCAGCGCTTGGATGCAAGACATTTACTTCGCAAGGATTTGGT	963
DB		

RESULT 10
 US-09-938-842A-2486
 ; Sequence 2486, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2486
 ; LENGTH: 1152
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-2486

Query Match	34.2%	Score	457;	DB	9;	Length	1152;	
Best Local Similarity	67.9%;	Fred.	No.	3.4e-332;	Indels	12;	Gaps	1;
Matches	659;	Conservative	0;	Mismatches	300;			

Qy	128	TCTGCATCATCGGGAGCGGTCCGCTGCCGACACGCGCAGCACTCATCGCGGCCCGCGCGG	187
Db	182	TTTTCATCGTCGGAAGTGGAACGACGACACACGCGCGCGCATCTATGTCATTCGAGACGG	241
Qy	188	AGCTCAAGCCTGTGCTCTTCGAGGGCTGGATGGCCAAACGACATCGCCGCGCGGGGGGCGAC	247
Db	242	AGCTTAAGCCTCTCTCTTCGAAGGATGGATGGCTAACGACATCGCTCCCGGGGTCAAT	301
Qy	248	TCACCACCAACGCGAGCTGAGAACTTCCGGGCTTCCCACAAGCGCATCATGGCGCGCG	307
Db	302	TAACTACAACAACCGAGTGGAAACTTCCCTGGGTCCCTTGAAAGGTATTCTCGGTATTG	361
Qy	308	ACCTCATGAGCAAATGCGCGCGCGAGTCCCTGCGCTTTGGCACCAACATCCTCTCCGAGA	367
Db	362	ATATGTTGAGAAATTCAGAAAAAATACTGGAGAGATTGGAACTTACGATCTTCAACGGAAA	421
Qy	368	CCGTACCGCGCTGCATCTTTTCGGCTGCCCATTCGAGTTTAGTGCAGACTCCAACAACG	427
Db	422	CTGTTAACAAGHTTGATTTCTATCGAAAACGTTTAAAGCTATTCACTGATTCGAGAACTG	481
Qy	428	TCCFCGCGGATPCGGTTATATGTTTCCACGGGAGCGCTCGCGCGGGCGCTCCACTTCCCGG	487
Db	482	TTTCGCGTGAATCTGTAAATATTTCTACTGGAGCTGTGCTPAAACGCTTAGACTTCACTG	541
Qy	488	GGTCCGATGCA-----TACTGGAAACCGCGGCATCTCCGCCCTGTGCGCTCTGTG	535
Db	542	GATCTGGTGAAGGTAAATGGTGGTTTTTGGAAATCGTGGTATCTCCGCTTGCTGCTGTTGCG	601

Db 64 TCTGATCATCGGAGCGGTCCTCCGCCCCACACAGCGCGCTACGCGCTCGAGCG 123
Qy 188 AGCTAAGCTGTGCTCTTCGAGGGCTGAGTGGCCAAACGACATCGCGCGGGGGGCGAGC 247
Db 124 AGCTAAGCGGATCTCTTCGAGGGCTGAGTGGCCAAACGACATCGCGCGGGGGGCGAGC 183
Qy 248 TCACCAACCAACCGAGCTGAGAACTTCCCGGGCTTCCCAACGGGCGATCATCGGGCGCG 307
Db 184 TCACCAACCAACCGAGCTGAGAACTTCCCGGGCTTCCCAACGGGCGATCATCGGGCGCG 243
Qy 308 ACTCATATGAGAACTGCGCGCGGAGCTGCTGCGCTTTTGGCAACATCTCTCCGAGA 367
Db 244 AGCTCATGGAACGCTGCGGAGCGAGCTGCTGCGCTTCCGCAACGAGATCCACCGAGA 303
Qy 368 CCGTCAACCGCGTGCAGCTTTTCGGCTGCGCCATTCGAGTTAGTGAGAGATCCACAAACCG 427
Db 304 CCGTCTCCAAAGTTCGATTTCTGAAACCGTCTCTTCAGGGTTTTCACCGATTCGGAACG 363
Qy 428 TCCTCCCGGATCGGTTATCTGTCGCAACGGAGCGGCTGCGCGGGCTCTCCATTCGCGG 487
Db 364 TCGAGCGCGAATCCGTATCGTGGCCACCGGTCGCTGCGCAAGCGGCTCTCCCTTCCCGG 423
Qy 488 GGT-----CGATGCTATCTGGAACCGCGCATCTCCGCTGTCGCGCTGCTGTG 535
Db 424 GCTCCGCGGACGCGCGGAGGCTACTGGAACCGTGGAACTCTCGCGCTGCGCTGTGCG 483
Qy 536 ACCTGCGCGCGCGCATCTTCCGTAACAGCCCATGCGCTCATAGCGCGGCGGAGCTCCG 595
Db 484 ACGCGCGCGCGCATCTTCCGTAACAGCCCATGCGCTCATAGCGCGGCGGAGCTCCG 543
Qy 596 CTATGAGGAGTCTCAATTTCTCACCAGTACGGCTCCACGCTTACATCATCCACCGCC 655
Db 544 CCATGAGGAGGACCATCTCTCACCAGTACGGCTCCACGCTTACATTAATTCACCGTA 603
Qy 656 GCAATACCTTCCGCTCTTCAAGATCATGAGGCGAGGCGCTTGAGAAACCCCAAAATTA 715
Db 604 GGAATAGTTCAGGGCTTCGAGATATGAGAGGATGATGATTAATAGTAAGATTA 663
Qy 716 AGTTCCTCTGGGACTCGGAATTTGTGAGGCTATGCGGCGGCA---AACGGGGGCGCAT 772
Db 664 AGGTGATTTGGAATTCGGTGTGTTGAGGCTTTTGGGGCGGAGATAACAGAGGGTGC 723
Qy 773 TGCGTGGCTAAAGTTAAGAACTACTGAATGTGAGGCTCGGATCTTCAGTGTCTG 832
Db 724 TTGGGGATTTGAGGTGAGAAATGCTGTGACTCAAGAGGTGTCTGAATTTGAAGTTTCTG 783
Qy 833 GCCTCTTTTGGCAATCGGCGATGAGCGCGGACCAAAATTCCTGGCGGAGACAGTTGAAAC 892
Db 784 GGTGTTTTCGCAATTTGGGCAACGAGCCCGGACCAAGTTCTTGGACGGGCGAGCTTGAAT 843
Qy 893 TCGATTCAGATGGTTATGCGGAACCAAGCCAGTTCCTCACTCACCAAGTGTAAAGGGTG 952
Db 844 TGGATTCGATGGATATATTGTGAGAGCGGGGACGACGAGACGAGTGTGAGGGAG 903
Qy 953 TATTGCTGCTGGGACGTCAGGACCAAGATACCGTCAGGCGCAATTAATTCGCGCTGGAT 1012
Db 904 TGTTTGTCTGGGATGTTTCAGGACCAAGATATAGGCAAGCTATTACTGCTCTGCA 963
Qy 1013 CAGGTCATGCGCTGCAATGAGCGCTGAGCACTACCTCGAGGAGATCGGTGCAAGGAG 1072
Db 964 CTGATCATGCGCTGCTTGGATGCAACATTAACCTGCAAAATGTTGGTTTACACAG 1023
Qy 1073 GAAAGTCTGATTGACTATATT 1093
Db 1024 ATAAGATGATTGACTAGCTT 1044

RESULT 9
US-10-424-599-13171
; Sequence 13171, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 13171
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_1118C.1
US-10-424-599-13171

Query Match 36.0%; Score 481.4; DB 13; Length 964;
Best Local Similarity 69.9%; Pred. No. 6.4e-140;
Matches 689; Conservative 0; Mismatches 276; Indels 12; Gaps 1;
Qy 118 CGACGCGCATCTGATCATATCGGAGCGGTCCCGCTGCGCACACGCGAGCATCTACGGG 177
Db 7 CGTCCGAGCTCTGATCATATCGGAGCGGCGGCGGCGCACACGCGCGCCATATACGGG 66
Qy 178 GCCCGGCGAGCTCAAGCTCTGCTCTTCGAGGGCTGATGCGCAACGACATCGCGCG 237
Db 67 GCGCGGCGGAGTGAAGCGGCTCTCTTTGAAGGCTGATGCGCAACGCGTCTGCTCC 126
Qy 238 GCGCGGAGCTCACCAACCAACGAGCTCGAGAACTTCCCGGGCTTCCCAACGCGATC 297
Db 127 GGTGGCGAGCTCACCAACCAACGAGCTCGAGAACTTCCCGGGATTTCCCGCGGATC 186
Qy 298 ATGGGCGCGAGCTCATATGAGCAACTGCGCGGCGGAGTCCCTCGGCTTTCGCGCAACATC 357
Db 187 CTGGCACCGAGCTCATGACCGCTGCGCGGAGCTCGCAACGCTTTCGCGCGGAGTA 246
Qy 358 CTCTCGGAGACCTCACCGCGCTCGAGCTTTTCGCGCTGCGCATTCGAGTTAGTGAGAC 417
Db 247 GTACGAGAGCGCTCACCGCGCTCGACCTCTCCACAGCTCCGTTTAGGGTTTACTCCGAC 306
Qy 418 TCACAAACGCTCTCGCGCATATGCGGTATCTGTTGCAACGAGCGCTTCGCGGCGGCTC 477
Db 307 TCCACCAACGCTGAGGCGGAGTCCCGTGGTGGTGGCGCGGCTGTGGCGAAGCGCTT 366
Qy 478 CACTTCCCGGGTCC-----GATGATATCTGGAACCGCGGCTCTCCGCTGT 525
Db 367 AATTTCATGAGCGCGGTCACACCTCGAGCGGTTCTGNAACGCGGCATATCCGCGTGC 426
Qy 526 GCGCTCTGAGCGGTGCGCGCGGCTTCCTCGTAAACAGCCCATCGCCGCTCATAGCGGC 585
Db 427 GCTGTGTGCGACGCGCGCGCCCAATATTCCGCGGCAACCCGCTGCTGTGATTCGCGCGC 486
Qy 586 GCGGACTCGGCTATGAGGAGTCCAAATTTCTCACCAAGTACGCGCTCCCAACGCTACATC 645
Db 487 GCGGATTCGCGATGAGGAGAGTACTCTCTCTCCAGTTTGGCTTCAAGGTTGATACATA 546
Qy 646 ATCCACCGCGCAATACCTTCGCTGCTCAAGATCATCGAGCGCAGGGCGCTTGAGAAC 705
Db 547 ATTCATAGGAGGCAAGTTTAGGGCTTCTAAAGTCAATGAGGAAAGGTGATGATAAT 606
Qy 706 CCCAAATTAAGTCTCTGCGGAGTTCGAGGTTGTCGAGGCTTATGCGCGCAACCGC 765
Db 607 CCCAAATTAAGTGTGTGGAAATTCAGTGGTGGTGGGCTCTGCGGATGATAGGGT 666
Qy 766 GGCCCATTCGCTGGCGTAAAGGTTAAGAACTTGAAGTGAAGTGTGGTCACTGGGCTGTCTGATTGAAG 726
Db 667 AGGATTTCTGGAGGGTTAAGGTTGAAGTGAAGTGTGGTCACTGGGCTGTCTGATTGAAG 726
Qy 826 GTGCTGGGCTCTTCTTGGCGCATGAGCGCGGACCAAAATTCCTGGCGGACAG 885
Db 727 GTTCTGGAATTTGTTCTTTGCAATTGGGCATGAGCGCTGCGCAAAAGTTCTTGGATGTCAA 786

QY 871 TTCTGGGGGAGAGCTTGAATCTGATTCAGATGTTATGTGAAACCAAGCCAGGTTCC 930
DB 780 TTCTCAATGGGAGCTTGGATCTCCATGSCGATGGTATGTGGCCACCAAGCCGGCTCT 839
QY 931 ACTCACACAGTGTAAAGGTTATTTCTGCTGGGAGCTGCAGACAGAGTACCGT 990
DB 840 ACACATACAGTGTGGAGGG-GTCTTTGCTGTGGAGAGCTGCAGATGAAGTATCT 898
QY 991 CAGGCCATTACTGCCCTCGATCAGGGTGCATGGCTTGCAATT-GGAGCTTGAGCACTACT 1049
DB 899 CAGGCCATTACTGCTGTGATCAGCTTCATGGCTGCTTTGGAGCGCGAGCACTATCT 958
QY 1050 GAGGAGATCGGTGCACAGAGGAGGAAGTCTGATTGA 1086
DB 959 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

RESULT 4
US-10-091-841-23
; Sequence 23, Application US/10091841
; Publication No. US20030150010A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: NADP-Thioredoxin and
; TITLE OF INVENTION: Barley Gene for Thioredoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/10/091,841
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 09/540,014
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-091-841-23

Query Match 55.3%; Score 738.6; DB 15; Length 995;
Best Local Similarity 85.8%; Pred. No. 1.5e-220;
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;
QY 91 ATGGAGGATCCCGCGGCTCCGCTCCGACCGGATCTGCATCTCGGAGCGGTCC 150
DB 1 ATGGAGGATCCCGCGGCTCCGCTCCGACCGGCTGCATCTCGGAGCGGCGCG 60
QY 151 GCTGGCGACACGCGAGCATCTACGGCGCGCGCGGAGCTCAAGCTGTGCTTTCGAG 210
DB 61 GCGCGCACACGCGGCGCATCTACGGCGCGCGCGGAGCTCAAGCGGTCTTCGAG 120
QY 211 GGCTGATGCGCAACGATCGCGCGCGGCGGAGCTCACACACGACCGAGCTCGAG 270
DB 121 GGCTGATGCGCAACGATCGCGCGGCGGCGGAGCTCACACACGAGCTCGAG 180
QY 271 AACTTCCCGGGTTCCTCCCAACGGCATCATGGGCGCGGACCTCATGACCACTCGCGCG 330
DB 181 AACTTCCCGGATTCCTCCCGCGGATCATGGGCGGATCGACCTCATGACCACTCGCGCG 240
QY 331 CAGTCCCTGGCTTTGGGACACATCTCTCCGAGACCGTCAAGCGGCTTCGATTCG 390
DB 241 CAGTCCCTGGCTTTGGGACACATCTCTCCGAGACCGTCAAGCGGCTTCGATTCG 300

QY 391 GCCTGCCCATTTCCAGTTAGTGCAGACTCCACAAACCGTCTCTCGCGGATCGGTTATCGTT 450
DB 301 GCCCGCCCTTTCCCGCTCACCTCCGACTCCACCAACCGTCTCTCGCGGACACCGTCTGCTC 360
QY 451 GCCACGGGAGCGCTCGCGGCGGCTCCACTTTCCCGGCTCCGATGCATCTCGAAACCGC 510
DB 361 GCCACGGGAGCGCTCGCGGCGGCTCCACTTTCTCCGGTCCGACACCTACTCGAAACCGC 420
QY 511 GGCACTCCCGCTCTGCGGCTCTGTGAGAGGTGCGCGGCTCCATCTTCGTAACAGCCCATC 570
DB 421 GGCACTCCCGCTCTGCGGCTCTGTGAGAGGTGCGCGGCTCCATCTTCGGAACAAGCCCATC 480
QY 571 GCCGTCAAGCGGCGGCGGCTCCGCTATGAGAGGTCCAAATTTCCCTCACCAAGTACGGC 630
DB 481 GCCGTCAAGCGGCGGCGGCTCCGCTATGAGAGGTCCAAATTTCCCTCACCAAGTACGGC 540
QY 631 TCCCAAGTCTACATCATCCACCGCGGCAATCTTCGCTGCTTCAAGATCATGAGGCGC 690
DB 541 TCCCAAGTCTACATCATCCACCGCGGCAATCTTCGCTGCTTCAAGATCATGAGGCGC 600
QY 691 AGGGCGTTGAGAACCCCAAAATTAAGTCTCTTGGGACTCGGAAGTGTGAGGCGCTAT 750
DB 601 AGGGCGTTCTCAATCTCAAGTCCAGGTTGTCTGGGACTC-GAGGTCTGAGGCTTAC 659
QY 751 GCGGCGCAAAACGGCGGCGGCTTGGCTGGCGTAAAGGTTAAAGAACCTACTCAATGCTGAG 810
DB 660 GCGGCGGAGCGGCGGCGGCTTGGCTGGCGTAAAGGTTAAAGAACCTACTCAATGCTGAG 719
QY 811 GTCTCGATCTTCAAGGTTCTGGGCTCTTCTTCCGCTCGGAGTGTGAGGCGCTTAC 870
DB 720 GTCTCGATCTTCAAGGTTCTGGGCTCTTCTTCCGCTCGGAGTGTGAGGCGCTTAC 779
QY 871 TTCTCTGGCGGACAGCTTGAATCGATTCAGATGCTTATGTGGAACCAAGCCAGGTTCC 930
DB 780 TTCTCTAGTGGGAGCTTGGATCCATCGCGATGGTATGTGGCCACCAAGCGGCTCT 839
QY 931 ACTCACACAGTGTAAAGGTTATTTCTGCTGGGAGCTGCAGACAGAGTACCGT 990
DB 840 ACACATACAGTGTGGAGGG-GTCTTTGCTGTGAGAGCTGCAGATGAAGTATCT 898
QY 991 CAGGCCATTACTGCCCTCGATCAGGGTGCATGGCTGCAATT-GGAGCTTGAGCACTACT 1049
DB 899 CAGGCCATTACTGCTGTGATCAGCTTCATGGCTGCTTTGGAGCGCGAGCACTATCT 958
QY 1050 GCAGGAGATCGGTGCACAGGAGGGAAGTCTGATTGA 1086
DB 959 GCAGGAGGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

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; Sequence 26, Application US/10306292
; Publication No. US20030145347A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gasdaska, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; TITLE OF INVENTION: THEREIN
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/10/306,292
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: US/09/598,747
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-306-292-26

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QY	185	CGGAGCT	CACGCTG	GTGCTCT	TTTCAG	GGGCTCG	ATGG	CCAA	CGACAT	CGCGCG	CGGGCGGGC	244	
DB	181	CGGAGCT	CACGCTG	TGCTCT	TTTCAG	GGGCTCG	ATGG	CCAA	CGACAT	CGCGCG	CGGGCGGGC	240	
QY	245	AGCTCAC	CAACCA	CCGAC	CGTCG	AGAACTT	CCCG	GGCTT	CCCCAA	CGGACAT	ATGGGGC	304	
DB	241	AGCTCAC	CAACCA	CCGAC	CGTCG	AGAACTT	CCCG	GGCTT	CCCCAA	CGGACAT	ATGGGGC	300	
QY	305	CGGACCT	CATGGAC	CAACTG	CCCG	CGCGAG	TCCT	CGCTTT	GGCAC	CAACAT	CTCTCTCCG	364	
DB	301	CGGACCT	CATGGAC	CAACTG	CCCG	CGCGAG	TCCT	CGCTTT	GGCAC	CAACAT	CTCTCTCCG	360	
QY	365	AGA	CCGTC	CACCG	CGTGC	ACTTTT	TCGG	CTCC	CCATTT	COGAGT	TAGTCG	ACAA	424
DB	361	AGA	CCGTC	CACCG	CGTGC	ACTTTT	TCGG	CTCC	CCATTT	COGAGT	TAGTCG	ACAA	420
QY	425	CGGTCTC	CGCGAT	CGGTAT	CGTTGCC	ACGG	AGCG	CGTTCG	CGGGG	CGCTCC	CACTTCC	484	
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QY	485	CGGGT	TCGATG	CATCTG	GAAAC	CGCG	GCATCT	CCGCT	GTGCG	CTGTG	GAACG	GTCCG	544
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QY	665	TCG	TGCTT	CCAAG	ATCAT	TG	CAGC	CGGG	CGT	TGA	AAATTT	TAAGT	724
DB	661	TCG	TGCTT	CCAAG	ATCAT	TG	CAGC	CGGG	CGT	TGA	AAATTT	TAAGT	720
QY	725	GGG	ACTCG	GAATTT	TGTC	GGG	AGCTT	ATG	CGG	CGG	CGCCAT	TGCTGG	784
DB	721	GGG	ACTCG	GAATTT	TGTC	GGG	AGCTT	ATG	CGG	CGG	CGCCAT	TGCTGG	780
QY	785	AGGTT	TAAGAA	CC	TACT	GAAT	GGT	GAGG	GTCT	CG	ATCTT	CGGCT	844
DB	781	AGGTT	TAAGAA	CC	TACT	GAAT	GGT	GAGG	GTCT	CG	ATCTT	CGGCT	840
QY	845	CAATCG	GGG	CAATG	ACCG	CGG	ACCA	AAATTC	TTC	GGG	CGG	ACCTTGA	904
DB	841	CAATCG	GGG	CAATG	ACCG	CGG	ACCA	AAATTC	TTC	GGG	CGG	ACCTTGA	900
QY	905	GTTAT	TG	GGAA	CAAG	CCAG	GTTC	CACT	CA	CCAGT	GTATAA	GGGTAT	964
DB	901	GTTAT	TG	GGAA	CAAG	CCAG	GTTC	CACT	CA	CCAGT	GTATAA	GGGTAT	960
QY	965	CGG	AGTC	CGG	ACAA	GAAGT	ACCGT	CAGG	CCATTA	CTG	CGCT	TGGAAT	1024
DB	961	CGG	AGTC	CGG	ACAA	GAAGT	ACCGT	CAGG	CCATTA	CTG	CGCT	TGGAAT	1020
QY	1025	CTGC	ATTGG	ACG	CTAC	CTTCG	AGG	AGAT	CGGTG	CA	CAGG	AGAA	1084
DB	1021	CTGC	ATTGG	ACG	CTAC	CTTCG	AGG	AGAT	CGGTG	CA	CAGG	AGAA	1080
QY	1085	GACT	TATAT	TTAG	GTAT	AGCA	ATCC	AT	CGAAT	PAGT	CAGT	GTG	1144
DB	1081	GACT	TATAT	TTAG	GTAT	AGCA	ATCC	AT	CGAAT	PAGT	CAGT	GTG	1140
QY	1145	CGG	CTCT	CGAT	GGCG	TTTAT	GC	ATGG	GTG	CTC	AGG	ATAC	1204
DB	1141	CGG	CTCT	CGAT	GGCG	TTTAT	GC	ATGG	GTG	CTC	AGG	ATAC	1200
QY	1205	TGA	TTATG	CTG	CTT	PAG	CA	AGT	CTAT	TTCT	TAT	CGTT	1264

[illegible]

GenCore version 5.1.6
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Run on: May 5, 2004, 23:26:46 ; Search time 618.786 Seconds
(without alignments)
9766.461 Million cell updates/sec

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Perfect score: 1336
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1322	99.0	1325	13	US-10-425-114-3716 Sequence 3716, Ap
2	1286	96.3	1286	13	US-10-425-114-5073 Sequence 5073, Ap
3	738.6	55.3	995	15	US-10-091-841-10 Sequence 10, Appl
4	738.6	55.3	995	15	US-10-091-841-23 Sequence 23, Appl
5	708	53.0	1560	15	US-10-306-292-26 Sequence 26, Appl
6	562.8	42.1	1021	15	US-10-306-292-24 Sequence 24, Appl
7	558.2	41.8	1645	13	US-10-424-599-65583 Sequence 65583, A
8	553.4	41.4	1284	13	US-10-425-114-29681 Sequence 29681, A
9	481.4	36.0	964	13	US-10-424-599-13171 Sequence 13171, A
10	457	34.2	1152	9	US-09-938-842A-2486 Sequence 2486, Ap
11	457	34.2	1152	11	US-09-938-842A-2486 Sequence 38, Appl
12	440.6	33.0	6357	13	US-10-290-072-38 Sequence 38, Appl
13	440.6	33.0	6357	15	US-10-141-531-37 Sequence 37, Appl
14	435.8	32.6	6357	13	US-10-290-072-43 Sequence 43, Appl

15	435.8	32.6	6357	13	US-10-290-072-45	Sequence 45, Appl
16	435.8	32.6	6357	15	US-10-141-531-43	Sequence 43, Appl
17	435.8	32.6	6357	15	US-10-141-531-45	Sequence 45, Appl
18	434.4	32.5	1345	13	US-10-290-072-215	Sequence 215, Appl
19	434.2	32.5	6357	13	US-10-290-072-40	Sequence 40, Appl
20	434.2	32.5	6357	13	US-10-290-072-44	Sequence 44, Appl
21	434.2	32.5	6357	15	US-10-141-531-40	Sequence 40, Appl
22	434.2	32.5	6357	15	US-10-141-531-44	Sequence 44, Appl
23	434.2	32.5	6357	13	US-10-290-072-34	Sequence 34, Appl
24	432.6	32.4	6357	13	US-10-290-072-35	Sequence 35, Appl
25	432.6	32.4	6357	13	US-10-290-072-42	Sequence 42, Appl
26	432.6	32.4	6357	15	US-10-141-531-34	Sequence 34, Appl
27	432.6	32.4	6357	15	US-10-141-531-35	Sequence 35, Appl
28	432.6	32.4	6357	15	US-10-141-531-42	Sequence 42, Appl
29	431.8	32.3	3787	9	US-09-897-898-13	Sequence 13, Appl
30	431.8	32.3	3787	13	US-09-897-898-15	Sequence 15, Appl
31	431.8	32.3	3787	15	US-10-032-201B-22	Sequence 22, Appl
32	431.8	32.3	4546	9	US-09-897-898-15	Sequence 15, Appl
33	431.8	32.3	4546	13	US-09-897-898-15	Sequence 15, Appl
34	431.8	32.3	4546	15	US-10-032-201B-24	Sequence 24, Appl
35	431	32.3	6357	13	US-10-290-072-29	Sequence 29, Appl
36	431	32.3	6357	13	US-10-290-072-30	Sequence 30, Appl
37	431	32.3	6357	13	US-10-290-072-37	Sequence 37, Appl
38	431	32.3	6357	13	US-10-290-072-39	Sequence 39, Appl
39	431	32.3	6357	13	US-10-290-072-41	Sequence 41, Appl
40	431	32.3	6357	13	US-10-290-072-46	Sequence 46, Appl
41	431	32.3	6357	15	US-10-290-072-46	Sequence 46, Appl
42	431	32.3	6357	15	US-10-141-531-29	Sequence 29, Appl
43	431	32.3	6357	15	US-10-141-531-30	Sequence 30, Appl
44	431	32.3	6357	15	US-10-141-531-37	Sequence 37, Appl
45	431	32.3	6357	15	US-10-141-531-39	Sequence 39, Appl
					US-10-141-531-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1

US-10-425-114-3716
; Sequence 3716, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 3716
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700336177_FLI
US-10-425-114-3716

Query Match 99.0%; Score 1322; DB 13; Length 1325;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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TGTAAATTCAGATTTCAGAGCGCGCAAGAACCTCTTGACCAACCGCGCGCGCGCGCGCA 60

Qy 65 AGCCAGCCCAACTGAGTAAAGAGTATGAGGAGTCCCGCGCGCTCCGCTCCGACCGC 124
AGCCAGCCCAACTGAGTAAAGAGTATGAGGAGTCCCGCGCGCTCCGCTCCGACCGC 120

172 CAGCGGTAC-----TGATCACCAGGATGGAAGAGCGGTGACCGACC 216
Db
253 ACCACACGAGTTCGAGACTTCGCGGCTTCCCAACGCGCATCATGGGCGCGACCTC 312
Qy
217 ACCACGAGGAGTTCGAGAACTTCGCGAGGATCGGAACGATCTCACCGGTCCGCTG 276
Db
313 ATGACAACTCGCGCGCGAGTTCCTGCGCTTGGCAACACATCTCTCCGAGACCGTC 372
Qy
277 ATGAGCGCATGCACGAGCATGCGCAAAATTCGAAACCGAGATCATTTTCGACCATATC 336
Db
373 ACCGCGTGCATTTTCGCGCTGCCATTCGAGTTAGTGAGACTCCACACCGTCTCTC 432
Qy
337 AGCGCGTGCATTTTCGCAAAACCGCGCTTTCGCTGACGAGCAGCGGAGTACACC 396
Db
433 GCCGATGCGGTTATCGTTGCCACGCGAGCGCTGCGCGCGCGCTCCATTTCCCGGGTCC 492
Qy
397 TGTGACGCGTATCATCGCACCGCGCTTCGCGCTTACCTGGGCGTGGCTTCCGAA 456
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493 GATGATATGGAACCGCGGCTATCTCCGCTGTCGCTGTCGAGTGGCGCGCGCCCATC 552
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457 GAAGCGCTTCAAAGCGCGCGCGCTTTCGCGCTGCGTACCTGGAGCG-----ATTCTTC 510
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553 TTCCTTAACAGCCCATCGCGCTCATAGCGCGCGCGCTTCGCTATGAGAGTCCAAAT 612
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511 TATCGCAACGAGAGTTCGCGGTATCGCGCGCGCGCAACCGCGAGTGGAGAGCTCTG 570
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613 TTCCTCAACAAGTTCGCGCTTCCGCTTACATCTACCGCGCGCGCAACCTTCGCTGCT 672
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571 TATCTGTGCAATATCGCTCTGAGGTACACCTGATCCACCGTGGGATTCCTTCGCTGCG 630
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673 TCCAGATATCATCGAGCGCGCGCTTCGAGAA-----CCCCAAAATTAAGTCTCTC 723
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691 ACCGATCGTACCTCGAAGAGTTCGCGCGCGCGAGTGGGCGTCAGCGCGCTGCGCGCTG 750
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751 CGCGATACCA-----AACHAGCAGCAATTCGAGTCCCTGGAAGTGGCTGTTATTGTC 807
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808 GCATCGGCGCACAGCGCGCAACCGCGCATCTTTGAGCGCGCAGCTGGAGCTGGAGAACCGC 867
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902 -----ATGTTATGTCGAACCGAGCGAGTTCCTCAACAGTGTAAAGGCTGTA 954
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1015 GGTGATGCTGCTGATGAGCTGAGCTGAGCTACCTGCGAGAGTGGTG 1063
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988 GGTGATGCTGCTGATGAGCTGAGCTTACCTGAGCGGTGGTG 1036
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RESULT 15

US-09-252-991A-14492/c
; Sequence 14492, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14492

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-14492

Query Match 12.4%; Score 165.4; DB 4; Length 666;

Best Local Similarity 58.0%; Pred. No. 1.9e-31;

Matches 343; Conservative 0; Mismatches 225; Indels 22; Gaps 2;

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Qy 182 CGCGGAGCTCAAGCTGTCTCTTCAGAGGTGATGGCGCAACGATCGCGCGCGCG 241

Db 572 CGGCAATCTCAAGCCAGTGTGTAT-----CACGGCATTCAGCCAGCG 528

Qy 242 GCGAGCTCACACACACCGAGCTTCGAGAACTTCCCGGCTTCCCAACGCGCATATGG 301

Db 527 GCGAGCTGACACACACCGAGTTCGAGAACTTCCCGGCTTCCCAACGCGCATATGG 468

Qy 302 GCGCGGACCTCATGGAACAATGCGCGCGGAGTCCCTGCGCTTGGCACCAAGATCTCT 361

Db 467 GCGCGGCGCTGATGACCGGATGCGAGCAGCGCGAGCGTTCGACACCGAGATCTCT 408

Qy 362 CCGGAGCGGTACCGCGCTGAGCTTTCGCGCTGCGCAATTCGAGTTAGTGCAGACTCCA 421

Db 407 ACGACCATCTCACACCGCGGAGTTCGAGAACTTCCCGGCTTCCCAACGCGCATATGG 348

Qy 422 CAACCGCTCTGCGGATGCGGTTATCGTTCGACGCGAGCGTTCGCGGCGCTTCCACT 481

Db 347 GCATTTATCTGCGATGCAATGATCATTTGCAACCGGTGCTCCGCGCAATACCTGGCA 288

Qy 482 TCCCGGCTCGATGATGCAATGCAACCGCGCATTCGCGCTGCGCTGCTGTCAGCGTG 541

Db 287 TGTGTCGGAAGAAGCTTTCATGCGGCAAGGCGTTCGCGCTGCGCTGCGCTGCGAGGT 228

Qy 542 CCGCGCGCATCTTCGCTAAACAGCCCATCGCGCTGCTGCTGCTGCGCGCGGCAATACCGCGCTG 601

Db 227 TT-----TCTACCGCAACCGAGTGTGCTGCTGCTGCTGCGCGCGGCAATACCGCGCTG 175

Qy 602 AGGAGTCAATTTCTCAGCAAGTACGCTCCGAGTCTACATCATCCCGCGCAATA 661

Db 174 AGGAAGCGCTGTACTTGGCCCAACATCGCAAGGAAGTCCACCTGATCCACCGTGGCA 115

Qy 662 CTTTCGCTGCTTCCAAAGATCATGCGAGCGCGGCTTGGAAACCCCAAA 712

Db 114 AGTTCGCTGCGAGAGATCTTCCAGGACAGCTGTTTCGACAGGCGCGAGA 64

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Job time : 125.208 secs

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OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
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FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 685:
SEQUENCE CHARACTERISTICS:
LENGTH: 1443 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...1443
US-09-221-017B-685

Query Match 15.1%; Score 202.4; DB 4; Length 1443;
Best Local Similarity 53.4%; Pred. No. 2e-40;
Matches 509; Conservative 0; Mismatches 421; Indels 24; Gaps 3;

Qy 122 CGCGATCTGCATATCGGAGCGTCCCGCTGCGCACGAGCGCATCTACGCGGCC 181
Db 1191 CACGCTGTCTCATCATCGGTTCCGACCTGCGCGGTATACGCGAGTATCTTCTC 1132
Qy 182 CGCGGAGCTCAAGCTGTCTCTTCCGAGGCTGGATGSCCAACGATCCCGCGGCG 241
Db 1131 GTGCCAATCTCAACCCATCTCTACGAGG-----ATACAAACCGCGCG 1087
Qy 242 GCGAGCTCACCACACACGAGCTCGAGAACTTCCCGGCTTCCCAACGCGATCATGG 301
Db 1086 GTACGTAACCACTACGACCGAGGTGGAAATCTTCCCGGTTATCCGAGGAATCAACG 1027
Qy 302 CGCGGAGCTCATGACAACTGCGCGGCGGAGTCCCTGCTTGGCACCAACATCTCT 361
Db 1026 GTACGAACTGATGGAAGACTTGGCAACAGCAACCCGCTTCCGAGCGGACATCGTT 967
Qy 362 CCGAGACCGTCAACCGCCCTGAGCTTTTCCGCTCGCCATTCCGAGTTAGTCAGACTCCA 421
Db 966 CGGGTATCGCTACAAAAGCGGATTTGACAAAGGCTCTTACAGGATCAAGATAGCGAG 907
Qy 422 CAACCG---TCCTGCGCATCGGTTATCGTTGACACGAGCGGCTGCGCGGCGCTCC 478

Db 906 AAAAGGAAATCAAGCCGATACGCTTATTTATCTCCACGGGTGCCACAGC-----CAAT 853
Qy 479 ACTTCCCGCGGTCGATGATATCGAACCGCGGATCTCCGCTGTGCGTGTGAGCG 538
Db 852 ACTTAGGCTTGGCGATGAGCCAAATATAGCCGGATGGTGTCTCTGTTGCTACCT 793
Qy 539 GTGCGCCCGCATCTTCCGTAACAAGCCCATCGCGTATAGCGCGCGGAGCTCCGCTA 598
Db 792 GTGATGGATTTTCTATCGCAAGAAGATAGCCGTAGTGGCGGAGGTGATGCTT 733
Qy 599 TGGAGGAGTCCCAATTTCTTCAACAGTACGGTCCCACTCTACATCATCCACCGCGCA 658
Db 732 GCGAGAGGCTCTCTATCTGGCATCGTGGCTGAACACGTTACCTGATCGTACGAAGA 673
Qy 659 ATACCTTCCGCTGCTCCAAAGATCATCAGGCCAGGCGCTTGGAGAACCCCAAAATTAAGG 718
Db 672 ACTATCTCGTGCCTCCAAAGTAAATGACGAGAGCGTGTGATGAATACGGGGAACATAACCG 613
Qy 719 TCCTCTGGGACTCGGAAGTTGTCAGGCTATGCGCGCGCAACACGGCGGCCCATTTGGCTG 778
Db 612 TTCTCTCGAACAATAATACGTTGGTCTATTCCGCGAAACGGTGTGGAAGGTGCTCATC 553
Qy 779 GCGTAAAGGTTAAGAACCTACTGAATGGTGAAGTCTCGGATCTTCAGGTGTCTGGCTCT 838
Db 552 TGGTGAACCGCAAGAGGAGCGCGACGAGAGATGGTGGACATTGCCATCGATGGTTTT 493
Qy 839 TCTTCGCAATCGGCGATGAGCGCGGACCAATTCCTGGCGGACAGCTTGAACCTCGATT 898
Db 492 TCCTCGTATCGGTATACGCAACTCGAAGATCTTCGCGGACTACCTCGACTTGGACG 433
Qy 899 CAGATGTTATGTGAAACCAAGCCAGGTTCCACTCACACACAGTGTAAAGGGTGTATTTG 958
Db 432 AAGTGGTTATATCTTGCAGGAGTTCTGCCCGCGCACAAAGTTCCCGGCGTATTTG 373
Qy 959 CTGCTGCGACGCTGACGACAGAAAGTACGTCAGGCCATTACTCGCTTGGATGAGGCT 1018
Db 372 CTGCGCGGACGTTGCCGACCCACACTATCTGTCAGGCTATCACGGTTCGCGGATAGGTT 313
Qy 1019 GCATGCTGCTATGAGCGCTGAGCACTACTCTGAGGAGATCGGTGCACAGGAGG 1072
Db 312 GCAAGCTGCTATCGAAGCAGAGCGTTATTGGCGGACGACGCTCTATATAAAG 259

RESULT 14
US-09-489-039A-4925
; Sequence 4925, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4925
; LENGTH: 1050
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-4925

Query Match 13.3%; Score 178.2; DB 4; Length 1050;
Best Local Similarity 53.6%; Pred. No. 1.6e-34;
Matches 509; Conservative 0; Mismatches 398; Indels 42; Gaps 5;

Qy 133 ATCATCGGAGCGTCCCGCTGCGCACGAGCATCTACGCGGCCCGCGGAGCTC 192
Db 112 ATCTTGTGTTCTGAACTTGGGATACACCGCGGCTCTATGCGCACGCGCACTG 171
Qy 193 AAGCTGTGCTCTTCGAGGCTGGATGGCCAAAGCATCGCGCGGCGGAGCTCACC 252

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LOCATION: (600001)...(615000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (900001)...(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

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Query Match 15.8%; Score 211.6; DB 4; Length 1230025;
Best Local Similarity 54.8%; Pred. No. 1.2e-41;
Matches 499; Conservative 0; Mismatches 394; Indels 21; Gaps 3;
QY 133 ATCATCGGAGCGGTCCGCTCGCACAGCGGAGCCATCTACCGCGCCCGCGGAGCTC 192
DB 366578 ATTATTGTTTCAGTCCATCTGGATATACAGCGCAATTATGATCAAGAGCGCTTTG 366519
QY 193 AACCTGTGCTCTTCGAGGCTGGATGCCCAACGACATCGCCGCGGCGGCGGACCTCAC 252

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DB 366518 CATCTCTTTTATTGAGGGTTTT-----CTCTGGGATCTCTGGTGGCCAGCTTATG 366465
QY 253 ACCACCCGAGCTCGAGACTTCCCGGGCTTCCCAACGCGCATCGGGCGCGGACCTC 312
DB 366464 ACTCAACAGAAAGTTGAGATTTTCCAGGGTTTCTGAGGGATTTCTTGGCCAAACTT 366405
QY 313 ATGACAACTCGCCGCGCGAGTCCCTCGCTTTTGGCACCAACATCTCTTCCGAGACCGTC 372
DB 366404 ATGAATATATGAAGAGAGCGCTGTGCGGTTTGGGACCAAGACACTAGCTCAAGATATT 366345
QY 373 ACCGCGCTGACTTTTGGCCCTGCCATTCGAGTTAGTCAGACTCCACACCGCTCCTC 432
DB 366344 ATTTCCGTTAGATTTTCTCTGTCGCCCTTTTATTTTGAATCAAAAGAGAAACCTATTCT 366285
QY 433 GCCGATCGGTTTATCGTTTCCACGCGGAGCCGCTCGCGGGCGCCCTCCACTTCCCGGGTC- 491
DB 366284 TGTGATGCTGATCATAGCTACAGGAGCTTCTCTAAAGCTTTAGAAATTTCTTGGAGCA 366225
QY 492 -----CGATGCTACTGGAACCGCGGATCTCCGCTTGTGCGCTGTGCGCTGTGAGCGTCCGCC 546
DB 366224 GGAACGATGAATTTTGGCAAAAGAGTGACTCTCTTGTGCGCTTTCGATGGGGCTTCT 366165
QY 547 CCCATCTTCCGTAACAAGCCCATCGCGTCAATAGCGCGCGCGGACTCCGCTATGAGGAG 606
DB 366164 CCTATTTTAAATAAAGATCTTTTGTGATTGGGGAGGGGATTTCTGCTTTAGAGAA 366105
QY 607 TCCAAFTTCCCTCAACAGTACGGTCCCACTGCTACATFATCCACCGCGCAATACCTTC 666
DB 366104 GCTCTTTACCTGACTCGTTATGGAAGCCACGTATATGTAGTTTCATGCTAGAGATAA 366045
QY 667 CGTCTTCCAAAGATCATGCGGCGGCGGCTTCAGAACCCCAAAATTAAGTCTCTCTGG 726
DB 366044 CGGCTTCTAAAGCTATGGAAGCTTCGGCGGCAAAACATGAGAAATTTACATTTTATGG 365985
QY 727 GACTCGGAAGTTGTGAGGCGCTATGCGGCGGCAAAACGCGCGCCCAATGGCTGGCGTAAAG 786
DB 365984 AATAGCGAGATTGTAAATAATTTCTGGAGATAGCATGTTCTCGTTC-----CCTAGAT 365934
QY 787 GTTAAGACCTACTGATGTTGAGGTCTCGGATCTTCAGTGTCTGCGCTCTCTTCTGCC 846
DB 365933 ATTAAGAATGTTTCAGACTCAAGAATTTACAATGAGAGCTGCGGGGGTGTCTTTGCT 365874
QY 847 ATCGGCGATGAGCGCGCGGACCAAAATTTCTGCGCGGACAGCTTTGAACCTCGATTCA 365814
DB 365873 ATAGGCCATAGCCAAATACGGATTTTCTCGAGGACAGCTGACGTTAGATGAGTGGGC 365814
QY 907 TATGTGAAACCAAGCGAGGTTCCACTCAGCCAGTGTAAAGGGTGTATTTGCTGCTGGC 966
DB 365813 TATATTGTGACTGAGAAAGGAACGCTCCAGACTTCTGTCTCCCTGAGTATTTGCTGCTGGA 365754
QY 967 GACGTGCAGGCAAGAGTACCGTCAGGCCATTTACTCGCGCTGGATCAGGGTGCATGGCT 1026
DB 365753 GATGTTTCAAGATAGTACTATGCTCAGCGGTTACTTCTCGAGGAGGTGTTGTATAGCA 365694
QY 1027 GCATTGAGCGCTGA 1040
DB 365693 GCATTGAGCGCTGA 365680

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RESULT 13

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US-09-221-017B-685/c
; Sequence 685, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA

```

Tue May 11 16:02:12 2004

us-10-005-429-24.rni

Db 178 GCAGCTCACCAACACACGACGTCGAGAA-TTCCCGGGCTTCCCAACGCGCATCGG 236

Oy 303 CGCCGACCTCATGG 316

Db 237 CGCCGACCTCATGG 250

RESULT 12

US-09-198-452A-1/c

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)..(15000)

OTHER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature

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LOCATION: (585001)..(600000)
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NAME/KEY: misc feature

Db 281 CGATCACTCGCGCGCGCGCTGATGCGCGCTGATGCGGCTATCTCGATT 222

Qy 1055 AGATCGTGACAGGA 1070

Db 221 CGCTCTGATGACAGA 206

RESULT 10

US-09-252-991A-13278

; Sequence 13278, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 13278

; LENGTH: 972

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-13278

Query Match 16.2%; Score 216.2; DB 4; Length 972;

Best Local Similarity 54.2%; Pred. No. 7.1e-44; Indels 30; Gaps 3;

Matches 524; Conservative 0; Mismatches 413;

Qy 104 CCGCGCTCGCTCGCGCGCGCTGATGCGGAGCGCTCGCGTCCGCGCACACGG 163

Db 26 CGGATACCTCCGCGCGCGCGAGTGATCTCTCGCTCGCGTCCGCGGTACAGCG 85

Qy 164 CAGCCATCTACGGCGCGCGCGAGTCTGATCTGCTTCGAGGCTGATGCCA 223

Db 86 CGGCTGTCTACGCGCGCGCGCAACCTCAAGCGCTGCTGATCAGCGGATCGAGGCC- 144

Qy 224 ACGACATCGCGCGCGCGCGAGCTCACACACACCGAGCTGCGAGAACTTCGCGGCT 283

Db 145 -----GGCGGCGAGTTGACACACCGAGCTGATGCGGAGCGAGCGCT 190

Qy 284 TCCCGAACGCGATATGGGCGCGAGCTCTGACACACTGCGCGCGAGTCTCGCT 343

Db 191 ATCCCGACGCGCTGACCGCGCGCGCTGATGCGGAGCGAGCGAGCGCT 250

Qy 344 TTGCGACCAACATCTCTCGAGACGCTCACCGCGCTGCTTTTGGCGCTGCCATTC 403

Db 251 TCGAGCCGAGATCGTCTTGACCAATTCATGCGCTGAGACTGCGCGCAAGCGTTCA 310

Qy 404 GAGTTAGTGAGACTTCCACACCGTCTCGCGATGCGGTTATCGTTCCACGCGAGCG 463

Db 311 CCCTGCGCGCGCAATGCGACCTTACACCTGCGAGCGACTGATGCGCGCGGTCGCA 370

Qy 464 TCGCGCGCGCTCCACTTCCCGGTCGATGATGATGATGATGATGATGATGATGATG 523

Db 371 GCGCGCGCTACTCGGCTGCGGTCGAGAGCGGCTTCATGGGAGGCGGTTCGCGCT 430

Qy 524 GTGCGCTCTGAGCGTCCGCGCGCGCTCTTTCGCGTAAACAGCCCATCGCGTATAGCG 583

Db 431 GCGCCACTGCGAGCGT-----TTCTTCTACCGCAACCGGAGTGGCGGTGATGCGG 484

Qy 584 GCGCGACTCGCTATGAGGAGTCCATTTCTTCTCAGCAGTACGCTCCCGAGTCTACA 643

Db 485 GCGCGCAATACCGCTGTGCGAGAGCGCTGTACCTTGGCGCAATCGCGAGCGGTGACCC 544

Qy 644 TCATCCACCGCGCAATACCTTTCGCTTCCAAAGATCATGCGCGCGCGCGCTTGAGA 703

Db 545 TGGTGATCTGCTCGGCAAACTTCCGCGCGGAGAGAATTCCTCAGGACAGGTCGAGCGC 604

Qy 704 ACCCGAAAATTAAGSTCTCTGGGACTCGGAAGTTGTGAGGCTATGCGGCGCGCAAG 763

Db 605 GGGTGGCGGAGGCAAGATAGTCTCAAGCTCAACGCGGAGTCCATGAGTGTCTGGCG 664

Qy 764 GCGGCCCATTTGGCTGGGCTAAAGSTTAAGAACCTACTGATGCTGAGTCTCGGATCTTC 823

Db 665 AACGATGGGCGTCAACCGCGCTGCGCTGAAGACCCGCGATGGTGGCGCGAGGATCG 724

Qy 824 AGGTGCTGCGCTCTTCTTCCGCGCATGAGCGCGCATGAGCGCGCGCAAAATTCCTGGCGGAC 883

Db 725 CCGTGGATGGCATGTTCTGCGCATCGGCGCATCTCCCAATACCTCGCTGTTCGAGGCG 784

Qy 884 AGCTTGAATCGATTCAGATGGTTATGTGGAACCAAGCCAGGTT-----CCACTC 934

Db 785 AACTGGCGCTGAAGACCGCTTACCTGTGTGTCACCGCGCGCGGAGGCAACCGCCACG 844

Qy 935 ACACGAGTTAAAGGGTGTATTTCTGCTGCGGACGTCGAGCAAGAAAGTACCTCAGG 994

Db 845 CGACCAAGCTACCGGGTGTGTTCCGCGCGCGAGCTGGCGGACCACTCTACGCGCAGG 904

Qy 995 COATTACTGCGCGTGGATGAGGTCATGGTGTGATGCGATGCGAGCTGAGCACTACCTGCGAG 1054

Db 905 CGATCAGCTCGCGCGCGCTGCTGATGCGCGCGCTGATGAGGCGCTATCTCGATT 964

Qy 1055 AGATCGG 1061

Db 965 CCGCTCG 971

RESULT 11

US-09-313-294A-3512

; Sequence 3512, Application US/09313294A

; Patent No. 6476212

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Ito, Laura Y.

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

; FILE REFERENCE: PL-0017 US

; CURRENT APPLICATION NUMBER: US/09/313,294A

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 7600

; SOFTWARE: PERL Program

; SEQ ID NO 3512

; LENGTH: 251

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6476212 700611759H1

; NAME/KEY: unsure

; LOCATION: 4, 31, 60

; OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-3512

Query Match 15.9%; Score 213; DB 4; Length 251;

Best Local Similarity 97.2%; Pred. No. 2.7e-43; Indels 4; Gaps 3;

Matches 247; Conservative 0; Mismatches 3;

Qy 63 GAAGCCAGCCAACTGAGTAAGCAGCTATGAGGAGTCCGCGCGCTCCGCTCCGAC 122

Db 1 GAAGCCAGCCAACTGAGTAAGCAGCTATGAGGAGTCCGCGCGCTCCGCTCCGAC 60

Qy 123 GCGCATCTGCATCATCGGAGCGGTCCGCTCGGACACGAGCGCATCTAGCGCGCG 182

Db 61 GCGCATCTGCATCATCGGAGCGGTCCGCTCGGACACGAGCGCATCTAGCGCGCG 120

Qy 183 CCGGAGCTCAAGCTGTGCTCTTCGAGGCTTGGATGGCAACGATCGCGCGCGCG 242

Db 121 CCGGAG-TCAAGCTGTGCTCTTCGAGGCTTG--TGGCAACGATCGCGCGCGCG 177

Qy 243 GCAGCTCACCAACCAACGAGCTCGAGAACTTCGCGGCTTCCCGAGCATATGCG 302


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QY 830 CTGGCTCTTCTTCCGATCGGCGATGAGCGGACCAATTCCTGGCGGACAGCTTG 889
Db 944 ACGGCTCTTCTTACGCTGTGTGTCAGACCCCGCAGTGCTGTCTGAAGGCCAGCTTG 1003
QY 890 AACTCGATTCAGATGTTATGTGGAACCAAGCCAGGTTCCACTCACACCAAGTGTAAAGG 949
Db 1004 AACTCGAGACGAGGATACATCATCACCAAGCCGCTACTAGCTTCACTAAGCTCGAGG 1063
QY 950 GTGTATTTGCTGCTGCGAGCTGCGAGCAAGAACTACGTCAGGCCATTACTGCGCGCTG 1009
Db 1064 GTGTATTTGCTGCTGCGAGTGTGTGAGTAAGCGCTACCGTCAGGCTATCACAGTGGCG 1123
QY 1010 G 1010
Db 1124 G 1124

RESULT 7
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 17.1%; Score 229; DB 3; Length 4403765;
Best Local Similarity 57.0%; Pred. No. 1e-45;
Matches 534; Conservative 0; Mismatches 370; Indels 33; Gaps 5;

QY 132 CATCATCGGAGCGGTCCGCTGCGCACACGCGCATCATGCGCGCGGAGCT 191
Db 4394014 CGTTATCGGCTCGGTCCGCGGGGTACACTGGGCGCTCTAGCGCGCGCGTCCAGCT 4394073
QY 192 CAAAGCTGTGCTTTTCAGGCTGGATGGCCACGACATCGCGCGCGGCGGAGCTCAC 251
Db 4394074 GCGCGCGCTGTCTTCGAGCGCACGCTCTTTT-----GGCGGCGCGCTGAT 4394118
QY 252 CACCACCGAGCTCGAGAACTTCGCGGCTTCCCAACGCGCATCATGCGCGCGGAGCT 311
Db 4394119 GACCAACCGAGCTGGAGAACTTACCGGGATTTGCGACGCGATCACCGGTCCAGATT 4394178
QY 312 CATGCAAACTGCGCGCGCGAGTTCCTGCGCTTTGGCAACCAATCCTCTCCGAGACCGT 371
Db 4394179 GATGATGAGATCGCGCAACAGCGCTGCGATTCCGCGCGGAGCTCGTATGGAAGAGCT 4394238
QY 372 CACCGCGGT--CGACTTTTGGCTGCGCCATTCCG--AGTTAGTCAGACTCCACACCGGT 428
Db 4394239 CGAGTCGGTATCACTTACCGGCGCGTGTGAATCGTGTGTACCGCGAGACAGACCA 4394298
QY 429 CTTTCGCGGATCGGCTTATCGTTGCCACGGAGCGGCTGCGCGCGCGCTCCACTTCCCGG 488
Db 4394299 CCGGCGCGGAGCGGTGATCTGTCGAATGGCGGAGCGGACAGCTATCTGAGGTGCGCG 4394358
QY 489 GTCCGATGCTACTGGAACCGGCGATCTCCGCTGTGCGTGTGAGCGGTGCGCGCGCC 548

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Db 4394359 CGAACAGGAATFCTCGGGCGCGGGTGAGCTGCTGCGCCACCTGCGACCG-----ATT 4394412
QY 549 CATCTTCGTAACAGCCCATCGCGCTCATAGGCGGCGGAGCTCCGCTATGAGGAGTCC 608
Db 4394413 CTTCTTCGCGATCAGGACATCGCGCGCTCATCGGCGGGGTGACTCGGCAATGAGGAGAC 4394472
QY 609 CAATTTCTTCACCAAGTACGCTCCACAGCTCTACATCATCACCGCGCGCAATACCTTCG 668
Db 4394473 TACCTTCTGACCCGATTCTGCTCGAGTGTGACGCTGTGTCATCGCGCGAGAGTCCG 4394532
QY 669 TGCTTCAGAGTCAATGACAGCGCGCTTGAGAAACCCCAAAATTAAGGTCCCTCTGGGA 728
Db 4394533 GGCTTCCAAAATCATGCTCGATCGCGCGCGCAACAAACAGAGATACGTTCTCTCACCA 4394592
QY 729 CTCGGAAGTTCTCGAGGCTATGCGCGCGCAACCGCGCGCCATTGGCTGCGCTGTAAGGT 788
Db 4394593 CCACACCGTGTGCGGGTGGAGCGGACACCA-----CACTGACCGGCTTGGGGT 4394643
QY 789 TAAGAACCTACTGAATGTTGAGTCTCGGATCTTCAGGTGTCTGGCCCTCTCTTTCGCGAT 848
Db 4394644 ACGGACACCAACACCGGTGCCGAAACCACTCGCGGTAAACCGGTGTTTTCGTCGCGAT 4394703
QY 849 CGGCGATGAGCGCGCGACCAAAATTCCTGGGCGGACAGCTTGAACTCGAATCAGATGTTA 908
Db 4394704 CGGCCACGAGCGCGGTGCGGCTTGGTGGCGAGGCGCATCGAGTCCGCGAGCGCTA 4394763
QY 909 TGTGAAACCAAGCGAGGTTCCACTCACACAGTGTAAAGGTGTATTTGCTGCTGCGCA 968
Db 4394764 CGTGTGTGTCAGCGGCGGTACCAACAGCACCTCACTGCGCGGCGTGTTCGTCGCGCGCA 4394823
QY 969 CGTCAGGACAAAGTACCTGCTGAGGCGTACCTGAGGCGCTTACTGCGCGTGGATCAGGCTGC 1028
Db 4394824 CTTGTGTGTCGACCTATCCGAGGCGGTTACCGAGCGGCGTGTTCGTCGCGCGCGC 4394883
QY 1029 ATTGACGCTGACCACTTACCTGCGAGGAGATCGGTGCA 1065
Db 4394884 TATCGACCGGAGCGCTGGCTCGCGGACGACGACGA 4394920

RESULT 8
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 17.1%; Score 229; DB 3; Length 4411529;
Best Local Similarity 57.0%; Pred. No. 1e-45;
Matches 534; Conservative 0; Mismatches 370; Indels 33; Gaps 5;

QY 132 CATCATCGGAGCGGTCCGCTGCGCACACGCGCATCATGCGCGCGGAGCT 191
Db 4401778 CGTTATCGGCTCGGTCCGCGGGGTACACTGCGCGCTCTACGCGCGCTGTCGCCAGCT 4401837
QY 192 CAAAGCTGTGCTTCTTCGAGGCGTGTGATGCGCAACACATCGCGCGGCGGCGAGCTCAC 251
Db 4401838 GCGCGCGCTGTCTTTCGAGGCGCACTCTTTC-----GGCGGCGCGCTGAT 4401882

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Db 908 CATCACTCTCAGAACTGGTGATGCGAGCTTTGGATGCGAGCATTTACAGA 967
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Qy 1056 CATGGTGTCACAGGAGGAAGTCTGATTGA 1086
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Db 968 GATTGATCTCAGCAAGGTAAGAGTGATTGA 998
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RESULT 6

US-08-386-729A-6
; Sequence 6, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Rharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yossef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattavilder, Alfred
; APPLICANT: Fallissa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; TITLE OF INVENTION: production
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weill, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/0205
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1423 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Penicillium chrysogenum
; FEATURE:

; NAME/KEY: exon
; LOCATION: 119..140
; FEATURE:
; NAME/KEY: intron
; LOCATION: 141..223
; FEATURE:
; NAME/KEY: exon
; LOCATION: 224..1123
; FEATURE:
; NAME/KEY: intron
; LOCATION: 1124..1188
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1189..1271
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(119..140, 224..1123, 1189..1271)
; OTHER INFORMATION: /product= "HMW protein"
; OTHER INFORMATION: /gene= "trxB"
US-08-386-729A-6

Query Match 25.1%; Score 335.4; DB 1; Length 1423;
Best Local Similarity 62.8%; Pred. No. 4.1e-73;
Matches 566; Conservative 0; Mismatches 311; Indels 24; Gaps 2;
Qy 134 TCATCGGAGCGGTCCCGCTCGCGCACACGCGCAGCCATCTACGGCGGCCGCGGAGCTCA 193
Db 224 TTATTGCTCGGCGCTTGGTGCCACACTGCGCTATCTATCTATCGCGCGCAGAGCTCC 283
Qy 194 AGCTGTGCTTTCGAGGGGTGGATGGCCAAACACATCGCGCGGGGGGGGAGCTCACCA 253
Db 284 AGCCAGTCTTTACGAGGGGATGCTGCCAACAGGTACCGCGCGGGTGGTCAAGTCA 343
Qy 254 CCACACCGAGCTCGAGAACTTCCCGGGCTTCCCAACGCGCATCATGGGCGCCAGCTCA 313
Db 344 CGACCACTGAGTCGAGAACTTCCCGGATTCGCCAGCGCATCGCGCGGCGAGCTCA 403
Qy 314 TGGACAACTCCCGCGCGAGTCTCTGGCTTTGGCACAAATCTCTTCGAGACCTCA 373
Db 404 TGGACAACTCCCGCGCGCAATCCGAGCGCTTCGGCACCGGATCATCAGAGACCATCT 463
Qy 374 CGCGGTCGAGCTTTTCGGCTGCCATTCGAGTTAGTGCAGACTCCA----- 421
Db 464 CCAAGCTTGACCTCTCTCCCGGCCCTTCAAGATGGACCGAGTGGAGCATGACGAAG 523
Qy 422 -----CAACCGTCTCTCGCGAGTGGGTATCGTTGCGAGGAGCGTTCGCGGCG 472
Db 524 GCAGCGAGCGCGTCCGCGACCGCGCGCGCTCATTCATTCGCACAGCGCGCAACGCGCG 583
Qy 473 GCCTCCACTTCCCGGGTCCGATGATCTGGAACCGCGCATCTCGCTCTGCGCTCT 532
Db 584 GTCTGAACCTTCGCGCGAGGAGACCTTACTGGCAGAACGGAATCAGCGCTGTGCGCTCT 643
Qy 533 GTGACGCTGCGCGCGCCCATCTTCCGTAAACAGCCCATCGCGCTCATAGGCGGCGGACT 592
Db 644 GCGAGGTGCGGTGCCCAATTTTCGTTAACAAGCCCTGTACGTTATTGGCGGTGACT 703
Qy 593 CCCTATGAGGAGTCAATTTCTCTCAACAGTACGCTCCACGCTCTACATCATCAACC 652
Db 704 CCGCGCGCGAGGAGGCTGTTCTCGCGCAAGTACCGCGCAGCGCTGCTCTCTGCTTC 763
Qy 653 GCGCAATCTTCCGTCTTCAAGATCATGAGCGCGAGGCGCTTGAGAACCCCAAAA 712
Db 764 GCAAGGACAGCTGCGTGCCTTAACATCATATGCTGATCTCTCTGCGCCACCCCAAGT 823
Qy 713 TTAAGTCTCTGGGACTCGGAAGTTGTGAGGCGCTATGGCGCGGCAAA---CGGCGGCC 769
Db 824 GCAAGGTCCGCTTCAACACCGTCCCGCAGGCTTATCGCGCAGAGAACAGCCCTAAACGG 883
Qy 770 CATTGGCTGCGTAAAGGTTAAGAACTACTGAATGCTGAGGCTCTCGGATCTTCAGGTGT 829
Db 884 TCATGACCCACCTCCGTGTCAAGAGCTTCTCTCTAAACGCGGAGGAGGTGCTTGAGGCTA 943

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413 CAGACTCCCAACGCTCTCGCGATCGCGTTATCGTTCCACGCGGCGCTCGCGCGC 472
Db      |||
326 CGACTCCCAAGGCTATCTCGCGACGCGGTGATCTCGCCATCGCGCGCGTGGCAAGT 395
Qy      |||
473 GCCTCCACTTCCCGCGGTC-----CGATGCATCTGGAAACCGCGCATCTCG 520
Db      |||
386 GGCTCTCTCTCGTGGCTCGCGGAGTGCTCGCGCGCTCTGGAAACCGCGCATCTCG 445
Qy      |||
521 CTTGTGCGCTCTGTGAGCGTGGCGCGCCCATCTCTCGTACACGCGCCATCGCGTATAG 580
Db      |||
446 CTTGCGCTGTGTGCGAGCGCGCGCGCGCGATCTTCGCGCAACAGCGCGCTGCTGTGATCG 505
Qy      |||
581 GCGCGCGCGACTCGCTGTATGAGAGAGTCCAAATTCCTCAACAGTACGGCTCCCAAGTCT 640
Db      |||
506 GTGGCGGAGACAGCGCGATGGAGGAGGCAACTTCTCACCAAGTACGGCTCCAAAGTGT 565
Qy      |||
641 ACATCATCCACCGCGCGCAATACCTTCGTGCTCTTCCAGATCATGCGAGCGCGCGCTTG 700
Db      |||
566 ACATCATCCACCGCGCGCGCGCTTCGCGCGCTTCCAGATCATGCGAGCGCGCGCTCT 625
Qy      |||
701 AGAAACCCCAAAATTAAGTCTCTCGGACTCGGAGTGTGCGAGGCTATGCGCGCGCAA 760
Db      |||
626 CCAACCGGAGATCGAGTCACTTGAACTTCTTCTCGTGTGAGGCTTACGCGAGCGCG 685
Qy      |||
761 ACGGCGCGCCCATTTGGTGGCTAAAGTTAAGAACTTACCTGAAATGTGAGGTCTCGATC 820
Db      |||
686 AGCGGACGCTCTCGCGCGCTCAAGTGAAGAACTGTGTGACCGCGCGCTGTCGAGC 745
Qy      |||
821 TTCAGTGTCTGCTCTCTTCTCGCATCGGCGATGAGCGCGCGCAAAATCTCGGCG 880
Db      |||
746 TCAAGTGTCTGCGCTCTTCTTCTCGCATCGGCGCGCGCGCAAAATCTCTCGAGC 805
Qy      |||
881 GACAGCTTGAACCTCGATTCAGATGTTATGTGGAACCAAGCGAGGTTCACCTCACACCA 940
Db      |||
806 GCGGCGTGAGCTGAGCTCGAGCGCTACGTGTGACCAAGCGCGCGCAACCAAGACCT 865
Qy      |||
941 GTGTAAAGGTGTATTGTCTGCGGCACTGTGAGCAAGCAAGATGAGTACGTCAGGCCATTA 1000
Db      |||
866 CCGTGTCTGCGGTGTTTCTCGCGCGCGCGCGAGTGTGAGCAAGAGTACCGCGAGGCCATCA 925
Qy      |||
1001 CTGCGCTGTGATCAGCGGTGATGCTGCTATGAGCTGAGCACTACCTGCGAGGAGATCG 1060
Db      |||
926 CCGCGCGCGCGCGCGCTGATGCTGCGCGCGCGCGCTGAGCGCGCGCGCTACCTCCAGAGATCG 985
Qy      |||
1061 GTCCACAGGAGGAAGTCTGATT 1084
Db      |||
986 GCTCCAGCAGGCGCAAGTCCGACT 1009
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RESULT 5

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US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; TITLE OF INVENTION: NADP-Thioresdoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
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; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26
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Query Match 28.6%; Score 381.8; DB 4; Length 998;

Best Local Similarity 63.9%; Pred. No. 1.4e-84;
Matches 633; Conservative 0; Mismatches 342; Indels 16; Gaps 3;

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Qy 108 CGCTCCGCTCCGACGCGCATCTGCACTCATCGGAGCGGTCCCGTGGCGACACACGCGAGC 167
Db 12 CGAAACTCACAACACAGGCTCTGTATCGTAGGAAGTGGCCAGCGGACACACACGCGCGC 71
Qy 168 CATCTACGCGCGCGCGCGGAGCTCAAGCCTGTGCTCTTCGAGGCTGATGCGCGCAACGA 227
Db 72 GATTTACGCGAGTAGGCTGAACTTAAACCTTCTCTTCGAGGATGATGCTTACGA 131
Qy 228 CATGCGCGCGCGCGCGGAGCTTACCAACCAACGAGCTCGGAGAACTTCCCGGGCTTCC 287
Db 132 CATGCTCCCGGTGTCAACTCAACCAACCAACCC---GGTGAAGATTTCCCGGATTTCC 188
Qy 288 CAAACGCGATCATGCGCGCGCGGAGCTCATGCAAACTGCGCGCGCGAGTCCCTGCGCTTGG 347
Db 189 AGAAGGTATTCTCGGAGTAGAGCTCCTGACAAAATTCGTTAAACAAATCGGAGCGATTCG 248
Qy 348 CACCAACATCTCTCTCGGAGACGCTCACCGCGCTGACACTTTTCGGCTGCGCCATTCGAGT 407
Db 249 TACTACGATATTACAGAGACGCTGACGAACTCGATTTCTTCTGAAACCGTTTAAAGCT 308
Qy 408 TAGTCGAGACTCCACACCGTCTCTCGCGATGCGGTATCGTTGCGCAACGAGCGCGTTCG 467
Db 309 ATTCACAGATTCAAAGGCCATTCTCGCTGACGCTGTGATTTCTCGCTATTCGGAGCTGTGC 368
Qy 468 GCGGCGCTCCACTTCCCGGCTCGGATGCA-----TACTGGAACCGCGCGAT 515
Db 369 TAAGTGGCTAGTCTGTTGATCTGTGAGTCTCGAGGTTGTGGAACCGTTGAGT 428
Qy 516 CTCCGCTGTGCGCTGTGAGCGTGGCGCGCGCGCGCTTCCGTAAACAGCGCATCGCGT 575
Db 429 CTCCGCTGTGCTGTTTCGAGCGAGCTGCTCGGATATTCGCAACAAACCTCTTTCGCGT 488
Qy 576 CATAGCGCGCGCGAGCTCGCTATGAGGAGTCCAAATTTCTCACCAAGTACGCGTCCCA 635
Db 489 GATCGTGAGCGGATTTCTGCAATGGAAGAGCAAACTTCTTACAAATATGATCTAA 548
Qy 636 CGTCTACATCATCCACCGCGCGCAATACCTTCGCTGCTTCCAGATCATGCGAGCGCGAGC 695
Db 549 AGTGTATATATCGATAGGAGAGATGCTTTTAGAGCGTCTAAGATTATGCA-CAAGCGAC 607
Qy 696 GCTTGAAGAACCCAAATTAAGTCTCTGCGGACTCGGAACTGTCGAGGCTATGCGCG 755
Db 608 TTGTCTAATCCTAAGATTGATGTTGGAATTCGAACTGCTGTGTGGAAGCTTATGGA 667
Qy 756 CGCAACCGCGCGCCATTTGGCTGAGTAAAGTAAAGAACCTTACTGAATGTTGAGTCTC 815
Db 668 TGAAGAAAGAGATGCTTGGGAGATGCAAGTGAAGATGTGTTACCGGAGATGTTTC 727
Qy 816 GGATCTTCAGGTGTCTGCGCTCTTCTCGCATCGGCGATGAGCGCGCGCAACAAATTCCT 875
Db 728 TGATTTAAAGTTTCTGGAATGTTCTTTGCTATTGCTCATGAGCGAGCTACCAAGTTTT 787
Qy 876 GCGCGGACAGCTTGAATCGATTGATGTTGATGTTGTTGTTGTTGTTGTTGTTGTTGTT 935
Db 788 GGATGCTGCTGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 847
Qy 936 CACCAAGTGAAGGTTGATTTGCTGCTGCGGAGCTGCGAGCAAGAGATCCGTCAGCG 995
Db 848 GACTAGCGTTCGCGGAGTTTTCGCTGCGGCTGATTTTCAGGATAGAAATAGTAGCAAGC 907
Qy 996 CATTACTCGCTGCTGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1055
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Db 840 ACATACCAAGTGTGGAGG-GTCTTGTCTGGAGACGTGCAGGATAAGAGTATCGT 898
Qy 991 CAGGCCATTAATCGCTGATCAGGCTGCATGCTGCATT-CGAGCGTCACTACCT 1049
Db 899 CAGGCCATTAATCGCTGATCAGGCTGCATGCTGCATT-TGGAGCCCGCAGCACTACT 958
Qy 1050 GCAGGAGATCGTGCACAGGAGGAGAAAGTCTGATTGA 1086
Db 959 GCAGGAGTGGTGCACAGGCTGGCAGTCTGATTGA 995

RESULT 3
US-09-598-747-26
; Sequence 26, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gadsaaka, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-598-747-26

Query Match 53.0%; Score 708; DB 4; Length 1560;
Best Local Similarity 85.0%; Pred. No. 1.2e-164;
Matches 792; Conservative 0; Mismatches 140; Indels 0; Gaps 0;
Qy 87 AGCTATGAGGATCCGCGCGCTCCGCTCGACGCGCATCTGCAATCATCGGAGGG 146
Db 402 AGCCATGAGGATCCGCGGCGCCGCTCGACGCGCTGTGATCATCTCGGAGGG 461
Qy 147 TCCGCTCGCACAGGAGCATATACGCGGCCCGCGGAGCTCAAGCTGTGCTTT 206
Db 462 GCGTCCGCGCACAGGCGCGGATCTACGCGCGCGCGGAGCTCAAGCGCGTCTT 521
Qy 207 CGAGGCTGATGCGCAAGCATGCGCGGCGGCGGAGCTCACACACACCGAGT 266
Db 522 CGAGGCTGCTCGCAAGCATGCGCGGCGGCGGAGCTCACACACACCGAGT 581
Qy 267 CGAGAACTTCCCGGCTTCCCAAGCGCATATGCGGCGCGGAGCTCATGGAACCTGCCG 326
Db 582 CGAGAACTTCCCGGCTTCCCAAGGAGATCTCGCGGCGGAGCTCATGGAACCTGCCG 641
Qy 327 CGCGAGTCTTGGGACCAATCTCTCTCGAGACCGTTCAGCGCGTCACTT 386
Db 642 CGCGAGTCTTGGGACCAATCTCTCGAGACCGTTCAGCGCGTCACTT 701
Qy 387 TTCGCTGCTCCCAATTCGAGTTAGTGCAGTCTTCCCAAGCGCTTCCGCGGTTAT 446
Db 702 CTCGCGCGCTTCCGCTGCTCGAGTCTTCCCAAGCGCTTCCGCGGCTTCCGCGG 761
Qy 447 CTTTGCACGCGGAGCGTTCGCGGCGGCTTCACTTCCCGGCTCGATGCAATCTGAA 506
Db 762 CTTTGCACGCGGCGGCTTCCGCGGCGGCTTCACTTCCCGGCTCGATGCAATCTGAA 821
Qy 507 CCGCGGCTCTCGGCTGCGCTCTGTCAGCGGCTTCCGCGGCTTCCGCTTCCGCTTCCG 566
Db 822 CCGCGGCTCTCGGCTGCGCTCTGTCAGCGGCTTCCGCGGCTTCCGCTTCCGCTTCCG 881
Qy 567 CATCGCGCTCATAGCGGCGGAGCTTCCGCTATGAGGAGTCCAAATTCCTCACAAGTA 626
Db 882 CATCGCGCTCATAGCGGCGGAGCTTCCGCTATGAGGAGTCCAAATTCCTCACAAGTA 941

Qy 627 CGGCTCCCAAGTCTACATCATATCCACCGCGCGAATACCTTCGTCCTTCCAGATCATGCA 886
Db 942 CGGCTCCCAAGTCTACATCATATCCACCGCGCGAATACCTTCGTCCTTCCAGATCATGCA 1001
Qy 587 GGCAGGCGGCTTGAAACCCCAAAATTAAGGTCCTCGGACTCGGAAAGTTTGTCCAGGC 746
Db 1002 GGCAGGCGGCTTGAAACCCCAAAATTAAGGTCCTCGGACTCGGAAAGTTTGTCCAGGC 1061
Qy 747 CTATGCGGCGCAACCGGCGGCCATTTGCTGCGCTGAAAGTTTAAAGCTTCTGATGCG 806
Db 1062 CTATGCGGCGCAACCGGCTGAGGTCCTATTTGCTGCTGCTCAAGGTCGAGAACTTGTCT 1121
Qy 807 TGAGGCTCTGGATCTTCAGGTCCTGCGCTCTTCTTTCGCGCATCGGCGCATGAGCCGCGAC 866
Db 1122 GAAGATCTTCGACCTTCAGGTCCTGCGCTCTTCTTTCGCGCATCGGCGCATGAGCCGCGAC 1181
Qy 867 CAAATTCCTGCGCGGAGCAGCTTGAATCTGATTCAGATGCTTATGTGAAACCAAGCGAGG 926
Db 1182 GAAGTTCCTGCGCGGAGCAGCTTGAATCTGATTCAGATGCTTATGTGAAACCAAGCGAGG 1241
Qy 927 TTCGCTCAGCAGGCTGTAAGGCTGTATTTGCTGCGGAGCTGCGAGCTGCGAGCAAGTA 986
Db 1242 CTCGCGCACACAGGCTGTAAGGCTGTATTTGCTGCTGCGGAGCTGCGAGCAAGTA 1301
Qy 987 CCGTCAGGCGCATTAATCTGCGCTGCGATCAGGCT 1018
Db 1302 TCGCGAGCTTATTAATCTGCGCTGCGATCAGGCT 1333

RESULT 4
US-09-598-747-24
; Sequence 24, Application US/09598747
; Patent No. 6531648
; GENERAL INFORMATION:
; APPLICANT: Lananhan, Michael B.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Gadsaaka, Pamela Y.
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL
; FILE REFERENCE: A-31383P1
; CURRENT APPLICATION NUMBER: US/09/598,747
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-598-747-24

Query Match 42.1%; Score 562.8; DB 4; Length 1021;
Best Local Similarity 74.2%; Pred. No. 4.9e-129;
Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;
Qy 113 CGTCCGACGCGCATCTGATCATCGGAGCGGTCGCTGCGCACACGCGGCGCATCT 172
Db 26 CTCACAAACCGCGCTCTGATCTGCTGCTGCGGCTGCGCACACGCGGCGCATCT 85
Qy 173 ACGCGGCGCGCGGAGCTCAAGCTCTGCTTTCGAGGCGTGGATGCGCAACGACATCG 232
Db 86 ACGCGGCGCGCGGAGCTCAAGCTCTGCTTTCGAGGCGTGGATGCGCAACGACATCG 145
Qy 233 CCGCGGCGGCGGAGCTCACACACGCGGAGCTTCCCGGCTTCCCGGCGGAG 292
Db 146 CCGCGGCGGCGGAGCTCACACACGCGGAGCTTCCCGGCTTCCCGGCGGAG 205
Qy 293 GCATCATGCGGCGGAGCTCATGAGCAACTTCCCGGCGGAGCTTCCCGGCTTCCCGGCGG 352
Db 206 GCATCTCTGCGGAGCTGACGCGGAGCTTCCCGGAGGAGGCGGCTTCCCGGCGG 265
Qy 353 ACATCTCTTCCGAGCGGCTCACCGCGGCTGAGCTTTCGCGCTGCGGCTTCCCGGAGTAGTG 412
Db 266 CCATCTTCCGAGCGGCTGAGGAGGCTTCTCGAGCAAGCGGCTTCAAGCTCTTCA 325

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(without alignments)
6607.485 Million cell updates/sec

Title: US-10-005-429-24
Perfect score: 1336
Sequence: 1 gaactgaatttcagatttc.....cttagatatcaaaaaaaa 1336

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PCUS COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	738.6	55.3	995	4	US-09-540-014-10
2	738.6	55.3	995	4	US-09-540-014-23
3	708	53.0	1560	4	US-09-598-747-26
4	562.8	42.1	1021	4	US-09-598-747-24
5	381.8	28.6	998	4	US-09-540-014-26
6	335.4	25.1	1423	1	US-08-386-723A-6
7	229	17.1	4403765	3	US-09-103-840A-2
8	229	17.1	4411529	3	US-09-103-840A-1
9	217.2	16.3	1413	4	US-09-252-991A-12680
10	216.2	15.2	972	4	US-09-252-991A-13278
11	213	15.9	251	4	US-09-313-294A-3512
12	211.6	15.8	1230025	4	US-09-198-452A-1
13	202.4	15.1	1443	4	US-09-221-017B-585
14	178.2	13.3	1050	4	US-09-489-039A-4925
15	165.4	12.4	666	4	US-09-252-991A-14492
16	157.4	11.8	966	4	US-09-540-014-27
17	145.8	10.9	648	4	US-09-252-991A-15129
18	141	10.6	600	4	US-09-252-991A-14870
19	139.6	10.4	666	4	US-09-252-991A-14995
20	132.2	9.9	751	3	US-08-998-416-219
21	129.4	9.7	1020	4	US-09-543-681A-1461
22	123.2	9.2	49617	4	US-09-596-002-28
23	123.2	9.2	1830121	4	US-09-557-884-1
24	123.2	9.2	1830121	4	US-09-643-990A-1
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26	106	7.9	963	4	US-09-328-352-1552
27	88.8	6.6	933	4	US-09-134-000C-2109

ALIGNMENTS

RESULT 1

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US-09-540-014-10
; Sequence 10, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillau, Maxime
; APPLICANT: Lemauz, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresoxin and
; TITLE OF INVENTION: NADP-Thioresoxin Reductase
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 995
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-09-540-014-10

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Best Local Similarity 85.8%; Pred. No. 3.1e-172; Indels 3; Gaps 3;
Matches 855; Conservative 0; Mismatches 139;

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QY 151 GCTGCGACACGGGAGGCAATCTAGCGGCGCGCGGAGCTCAAGCTGTCTTTCGAG 210
DB 61 GCGCGCACACGGGCGGCAATCTAGCGGCGCGCGGAGCTCAAGCTGTCTTTCGAG 120
QY 211 GCCTGGATGGCAACGATCGCGCGGCGGAGCTCAACACACCGAGCTGCGAG 270
DB 121 GCCTGGATGGCAACGATCGCGCGGCGGAGCTCAACACACCGAGCTGCGAG 180
QY 271 AACTTCCGGGCTTCCCAACCGGATCATGCGGCGGAGCTCACTGGAACATGCGGCGG 330
DB 181 AACTTCCGGGATTTCCCAACCGGATCATGCGGCGGAGCTCACTGGAACATGCGGCGG 240
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Qy	1123	AGTCAGTTGCGGTGCTGAAAGCGGCTCTCTGATGCGCGTTTATGCAATGGGTGTGATG	1182
Db	228	AGTCAGTTGCGGTGCTGAAAGCGGCTCTCTGATGCGCGTTTATGCAATGGGTGTGATG	169
Qy	1183	AGCTCAGGATTCAGATACCTCGATGATTTATGCTGCTTAGTAGCATGCTATTCCTTATCGTT	1242
Db	168	AGCTCAGGATTCAGATACCTCGATGATTTATGCTGCTTAGTAGCATGCTATTCCTTATCGTT	109
Qy	1243	AGGATCCAGAGATATGTCGAAACCTCGAACTATTACTCGATACCTATTCGTCATTACTG	1302
Db	108	AGGATCCAGAGATATGTCGAACTCGAACTATTACTCGATACCTATTCGTCATTACTG	49
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Search completed: May 6, 2004, 01:11:49
Job time : 4017.94 secs

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Query Match 44.3%; Score 591.2; DB 14; Length 789;	
Best Local Similarity 89.4%; Pred. No. 2.3e-94;	
Matches 693; Conservative 0; Mismatches 74; Indels 8; Gaps 5;	
Qy 4 CTGTATTTTCAGATTTTCAGAGCGCGCAAG--AACCTCTTTGACCAACCGCGCGCGCGCG 61	
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Db 671 ACCTTCGCTGTTTCAAGATATGAGGCGCGCGCTTTGGAAAAAACCCANAAATAG 730	
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718 GTCTCTCGGACTCGGAA--GTTGTCGAGGCTATGGCGGCGCAACGCGGCGCC 770	
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LOCUS	
DEFINITION	
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VERSION	
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ORGANISM	
Zea mays	
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	
AUTHORS	
Walbot,V.	
TITLE	
Maize ESTs from various cDNA libraries sequenced at Stanford University	
JOURNAL	
COMMENT	
Unpublished (1999)	
Contact: Walbot V	
Department of Biological Sciences	
Stanford University	
855 California Ave, Palo Alto, CA 94304, USA	
Tel: 650 723 2227	
Fax: 650 725 8221	
Email: walbot@stanford.edu	
Plate: 606045 row: G column: 09.	
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Qy 1003 GCCGCTGGATCAGGGTGCAATGCTGCAATTTGGACGCTGAGCACTACTCCTCAGGAGATCGT 1062	
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QY 948 GGGTGTATTTGCTGTCGCGAGCTGCGAGCAAGAAAGTACCGTCAAGGCATTACTTGCCTGC 1007
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QY 1008 TGGATCAGGTCGATGGCTGCAATTCGAGCGCTGAGCACTACCTGACAGGAGTCCGCTGCACA 1067
DB 421 TGGATCAGGTCGATGGCGGCAATTCGAGCGCTGAGCACTACCTGACAGGAGTCCGCTGCACA 480
QY 1068 GGAGGGAAGTCTGATTCGACTATATTTAGGTGTAGCAACCAAGCAATCCATCGAATAGTCA 1127
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VERSION CC658777.1 GI:32062238
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 777)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGWP74TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
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Best Local Similarity 99.2%; Pred. No. 1.3e-95;
Matches 622; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

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CA228892.1 GI:35290862
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Saccharum officinarum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 789)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 058 row: F column: 10

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including seedlings treated with a variety of hormones

JOURNAL COMMENT

Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory

Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299

Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)

FEATURES

source

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callus, Cycloheximide-treated callus, Anaerobic treated
seedlings, NAA (a-Naphthalene acetic acid)-treated
seedlings, Kinetin-treated seedlings, ACP
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (Abscissic
acid)-treated seedlings, GA (Gibberellic acid)-treated
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molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
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NACTGGAGATTCCGGCCGCGCCAGCAATTTTCTTTTCTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
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synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

ORIGIN

Query Match 46.2%; Score 617.8; DB 12; Length 642;
Best Local Similarity 99.7%; Pred. No. 4.5e-99;
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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733 GAAGTTGTCGAGCCTATGCGCGCGCAACCGCGGCCCATTCGCTGGGCTAAGGTTAAG 792

582 GAAGTTGTCGAGCCTATGCGCGCGCAACCGCGGCCCATTCGCTGGGCTAAGGTTAAG 523

QY 793 AACCTACTGAATGTTGAGGTTCTGGATCTTTCAGGTGTTCTGCGCTCTTCTTGGCCATCGG 852
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RESULT 11

CA141638

LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CA141638 678 bp mRNA linear EST 24-SEP-2003
SCULRT2050E07.g RT2 Saccharum officinarum cDNA clone SCULRT2050E07
5', mRNA sequence.

CA141638

CA141638.1 GI:35035827

EST

Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

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Saccharum officinarum

Saccharum officinarum

Saccharum officinarum

Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
<http://www.bcccenter.fcav.unesp.br>
Plate: 050 row: E column: 07

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..678

/organism="Saccharum officinarum"

/mol_type="mRNA"

/db_xref="taxon:4547"

/clone="SCULRT2050E07"

Db 62 GAGGGAATCGCGCGGCTCCGCTCGGACGGGATCTGATCATCGGAGGGTCCGCT 121
Qy 154 GCGCACAGCGGAGCATCTACGCGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 213
Db 122 GCGCACAGCGGAGCATCTACGCGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 181
Qy 214 TGGATGCCACGACGATGCGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 273
Db 182 TGGATGCCACGACGATGCGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 241
Qy 274 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 333
Db 242 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 301
Qy 334 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 393
Db 302 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 361
Qy 394 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 453
Db 362 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 421
Qy 454 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 513
Db 422 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 481
Qy 514 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 573
Db 482 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 541
Qy 574 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 633
Db 542 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 601
Qy 634 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 656
Db 602 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGC 624

RESULT 9
CA830441
LOCUS
DEFINITION
1117006H07.y1 1117 - Unigene V from Maize Genome Project Zea mays
CDNA, mRNA sequence.
CA830441
VERSION
CA830441.1 GI:26558206
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 619)
Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1117006 row: H column: 07.
Location/Qualifiers
1. 619
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="dbEST:946118G10.y1"
/db_xref="taxon:4577"
/clone_lib="1117 - Unigene V from Maize Genome Project"

/note="This library represents the unique genes found in the fifth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from library 946. Contigs were assembled using ZmBAssembler and 2 representatives from each contig were selected for the Unigene set. All singlets were also selected."
Query March 46.3%; Score 619; DB 14; Length 619;
Best Local Similarity 100.0%; Pred. No. 2.7e-99; Indels 0; Gaps 0;
Matches 619; Conservative 0; Mismatches 0;
Qy 54 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 113
Db 1 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 60
Qy 114 GCTCCGACGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 173
Db 61 GCTCCGACGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 120
Qy 174 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 233
Db 121 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 180
Qy 234 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 293
Db 181 CGCGCGCGGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 240
Qy 294 CATCATGGGCGGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 353
Db 241 CATCATGGGCGGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 300
Qy 354 CATCTCTCCGAGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 413
Db 301 CATCTCTCCGAGAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 360
Qy 414 AGACTCCACAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 473
Db 361 AGACTCCACAGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 420
Qy 474 CTTCCACTTCCCGGGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 533
Db 421 CTTCCACTTCCCGGGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 480
Qy 534 TGAAGGTGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 593
Db 481 TGAAGGTGCGCGCGGAGCTCAAGCTGTGCTTTTCGAGGGCTGGATGGCCACGACATCGC 540
Qy 594 CGCTATGGAGGAGTCCCAATTTCTCAAGAGTACGCTCCACGCTTACATCATCATCATCAT 653
Db 541 CGCTATGGAGGAGTCCCAATTTCTCAAGAGTACGCTCCACGCTTACATCATCATCATCAT 600
Qy 654 CGCTATGGAGGAGTCCCAATTTCTCAAGAGTACGCTCCACGCTTACATCATCATCATCAT 672
Db 601 CGCTATGGAGGAGTCCCAATTTCTCAAGAGTACGCTCCACGCTTACATCATCATCATCAT 619

RESULT 10
BM351049/c
LOCUS
DEFINITION
BM351049 - E10.T3 ISUM5-RN Zea mays cDNA clone MEST272-E10 3', mRNA
sequence.
BM351049
ACCESSION
BM351049.1 GI:18175901
VERSION
BM351049.1
KEYWORDS
EST.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 642)
Wen,T.J., Guo,F., Guo,L., Ashlock,D.A and Schnable,P.S.
REFERENCE
Wen,T.J., Guo,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues

electroporated into DH10B. The total number of clones with insert was: zmrw05: 2.0x10⁷; zmrw48: 4.2x10⁷; zmrw00: 1.1x10⁷. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Heiao T C. Growth of the Maize Primary Root at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988. 50-57. (2) Spollen W G; Lenoble M E; Samuels T D; Bernstein N; Sharp R E. Abscissic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). March, 2000. 967-976.
TAG_TISSUE=Root _segment_2
TAG_SEQ=ACCGA"

ORIGIN

Query Match 47.5%; Score 635.2; DB 14; Length 659;
Best Local Similarity 98.6%; Pred. No. 3.8e-102;
Matches 640; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 678 GATCATGAGGCGGCGCTTGAAGACCCCAAAATTAAGTCCCTCGGACTCGGAAT 737
DB 659 GATCATGAGGCGGCGGCTGAGAACCCCAAAATTAAGTCCCTCGGACTCGGAAT 600
QY 738 TGTGAGGCGCTATGGCGGCGCAACCGGCGCCCATTTGGCTGGCGTAAGGTTAAGAACT 797
DB 599 TGTGAGGCGCTATGGCGGCGCAACCGGCGCCCATTTGGCTGGCGTAAGGTTAAGAACT 540
QY 798 ACTGAATGTTAGGTTCTGGATCTTCAAGTGTCTGGCTTCTTTCGCGATCGGCATGA 857
DB 539 ACTGAATGTTAGGTTCTGGATCTTCAAGTGTCTGGCTTCTTTCGCGATCGGCATGA 480
QY 858 GCGGCGGACCAATTCCTGGGCGGACAGCTTGAACCTCGATTCAGATGGTTATGTGGAAC 917
DB 479 GCGGCGGACCAATTCCTGGGCGGACAGCTTGAACCTCGATTCAGATGGTTATGTGGAAC 420
QY 918 CAAGCAGGTTCCATCACACAGTTAAAGGTTATTTGCTGCTGGCAGCTGCAGGA 977
DB 419 CAAGCAGGTTCCATCACACAGTTAAAGGTTATTTGCTGCTGGCAGCTGCAGGA 360
QY 978 CAAGAGTACCTGACGCGCTACTGCGCTGATCAGGTCGATGCTGCTGCTGCTGCTG 1037
DB 359 CAAGAGTACCTGACGCGCTACTGCGCTGATCAGGTCGATGCTGCTGCTGCTGCTG 300
QY 1038 TGAGCACTACCTGACGAGATCGGTGCACAGAGGGAAGTCTGATTCATATATTTAGG 1097
DB 299 TGAGCACTACCTGACGAGATCGGTGCACAGAGGGAAGTCTGATTCATATATTTAGG 240
QY 1098 TGTAGCAACCAATCCATCGATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1157
DB 239 TGTAGCAACCAATCCATCGATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 1158 CGCGTTTATGCCATGGTTGTCATGAGCTCACGATTGAGATACCTGATGATTATGCTGC 1217
DB 179 CGCGTTTATGCCATGGTTGTCATGAGCTCACGATTGAGATACCTGATGATTATGCTGC 120
QY 1218 TTAGTAGCATGCTATCTTATCTGTTAGGATCAGAGTATGCTGACTGCACTATTT 1277
DB 119 TTAGTAGCATGCTATCTTATCTGTTAGGATCAGAGTATGCTGACTGCACTATTT 60
QY 1278 ACTGGATACCTATCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1326
DB 59 ACTGGATACCTATCTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATC 11

RESULT 8
CKL44330
LOCUS
DEFINITION
3530.1.10.1 Col.V.11 3530 - Full length cDNA library created by
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
ACCESSION
CKL44330
VERSION
CKL44330.1 GI:38687299

KEYWORDS
SOURCE
ORGANISM

EST.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 624)

AUTHORS

Walbot, V.

TITLE

Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL

COMMENT

University
Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3530.1.10.1 row: C column: 01.
Location/Qualifiers
1. 624

FEATURES

source

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="multiple"
/dev_stage="varies by tissue"
/lab_host="DH10B"
/clone_lib="3530 - Full length cDNA library created by
Invitrogen from multiple tissues"
/note="Organ: silks, husks, ears, pollen, shoot tips,
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT
6.1; Site 1: EcoRV; Site 2: NotI; Zea Gene Discovery
Project contracted with Invitrogen to produce a
normalized, full length library in a pSPORT vector. This
is a Gateway compatible vector, permitting clone movement
to new vector backbones for expression in diverse host
cells using recombination rather than restriction enzymes.
Details of the vector and sequencing primers are available
at ZmDB in the EST library description tables. poly(A)+
mRNA was prepared by Invitrogen, and equimolar amounts of
RNA from each of the 12 tissue samples were mixed together
for selection of mRNA with a 5' cap. After synthesis of
cDNA, a normalization step was conducted against the
mixture of RNA sources. This step effected a 20X to 80X
reduction in common transcript types. Tissues prepared: 1.
just emerging silks; 2. inner husks from ears of sample
#1; 3. 20 dap aleurone; 4. immature tassels, stages from
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
vegetative shoot tips from 15 day old seedlings; all
leaves with an expanded or partially expanded sheath
were removed; 8. mature leaf tissue; 9. 0.5 cm long root
tips from 15 day old seedlings; 10. 10 dap whole seed; 11.
12 dap endosperm and embryo; 12. 17 dap endosperm and
embryo. All of the sequenced clones in project 3530 will
be archived at the University of Arizona along with the
Unigene clones from the Zea Gene Discovery EST
sequencing projects. Clones can be ordered through the
ZmDB web site or directly from the University of Arizona
(http://www.genome.arizona.edu/orders/). High density
filters containing over 18,000 clones can also be ordered
from the University of Arizona."

ORIGIN

Query Match 46.5%; Score 621.4; DB 14; Length 624;
Best Local Similarity 99.8%; Pred. No. 1e-99;
Matches 622; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 ACCCTCTTGACACCG 93
DB 2 AACCTCTTGACACCG 61
QY 94 GAGGATCCGCT 153


```

/lab host="XLOUP"
/clone_lib="946" - tassel primordium prepared by Schmidt
lab"
/notes=Organ: tassels; Vector: HybriZap; Site:1: EcoRI;
Site:2: XhoI; George Chuck dissected immature tassels
between 1mm and 3mm. Sharon Stanfield prepared the cDNA
library in HybriZap. Sample insert size range was 350 bp
to 3 kb with a 1 kb average.

```

ORIGIN

```
Query Match      48.0%; Score 641.4; DB 13; Length 643;
Best Local Similarity 99.8%; Pred. No. 3e-103;
Matches 642; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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57	QY	CGCGCGAGCCCAAGCCAAACTGAGTAAAGCAGCTATGGAGGGATCCGCGCGCGCTCGCT	116
1	DB	CGCGCGAAGCCCAAGCCAAACTGATTAAGCAGCTATGGAGGGATCCGCGCGCGCTCGCT	60
117	QY	CGCGACGCGCATCTGCATCATCGGAGCGGTCCGCTGCGCACACGCGACGCATCTACGC	176
61	DB	CGCGACGCGCATCTGCATCATCGGAGCGGTCCGCTGCGCACACGCGACGCATCTACGC	120
177	QY	GGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGATGCGCCAAACGACATCGCCGC	236
121	DB	GGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGATGCGCCAAACGACATCGCCGC	180
237	QY	GGCGCGGCGAGCTCACCAACAACGACGTCGAGAACTTCCCGGGCTTCCCAACGCGCAT	296
181	DB	GGCGCGGCGAGCTCACCAACAACGACGTCGAGAACTTCCCGGGCTTCCCAACGCGCAT	240
297	QY	CATGGCGCGGACCTCATATGACAACTGCGCGCGGCGAGTCCCTGCGCTTTGGCACCAACAT	356
241	DB	CATGGCGCGGACCTCATATGACAACTGCGCGCGGCGAGTCCCTGCGCTTTGGCACCAACAT	300
357	QY	CTCTCTCGAGACCGTCAACGCGCGTGCAGCTTTTGGCTGCGCCATTCGAGTTAGTGAGA	416
301	DB	CTCTCTCGAGACCGTCAACGCGCGTGCAGCTTTTGGCTGCGCCATTCGAGTTAGTGAGA	360
417	QY	CTCCAAACCGTCTCTCGCGAGTCGGGTATATCGTTGCCACGCGGAGCGGTTCGCGGGCGCCT	476
361	DB	CTCCAAACCGTCTCTCGCGAGTCGGGTATATCGTTGCCACGCGGAGCGGTTCGCGGGCGCCT	420
477	QY	CGACTTCCCGGGTCCGATGCCATCTGGAAACCGGCGCATCTCCGCTGTGCGCTCTGTGA	536
421	DB	CGACTTCCCGGGTCCGATGCCATCTGGAAACCGGCGCATCTCCGCTGTGCGCTCTGTGA	480
537	QY	CGGTGCGCGCCCCCATCTTCCGTAAACAGCCCATCGCGGTATAGCGGCGCGGACCTCCGC	596
481	DB	CGGTGCGCGCCCCCATCTTCCGTAAACAGCCCATCGCGGTATAGCGGCGCGGACCTCCGC	540
597	QY	TATGGAGGAGTCCAAATTTCTGTCACAGTACGGCTCCAGCTCTACATCATCCACGCGCG	656
541	DB	TATGGAGGAGTCCAAATTTCTGTCACAGTACGGCTCCAGCTCTACATCATCCACGCGCG	600
657	QY	CAATACCTTCCGCTCTCCAGATCATGCGAGGCCAGGGCGCTT	699
601	DB	CAATACCTTCCGCTCTTCCAGATCATGCGAGGCCAGGGCGCTT	643

RESULT 7	LOCUS	CF630838	659 bp	linear	EST 02-OCT-2003
		zmrw548	QB10-001-C08.s2	zmrw548	Zea mays cDNA, mRNA sequence.
		DEFINITION			

CP630838
ACCESSION
CP630838.1
VERSION
CP630838.1
KEYWORDS
GI:37387291
EST.

SOURCE: Zea mayr
Zea mayr
ORGANISM: Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 659)
REFERENCE: Bohnert, H., Sharp, R.E., Springer, G.K., Poroyko, V., Fredricksen, M.,

Sharp, L.G., Spollen, W.G., Ries, J., Guiller, A., Khambati, A., Topinka, C., Davis, G.E., Schachtman, D., Wu, Y., and Nguyen, H.T.
NSF Grant DBI-0211842: Functional Genomics of Root Growth and Root Signaling Under Drought
Unpublished (2003)
Contact: Hans Bohnert
University of Illinois, Urbana-Champaign
1201 West Gregory Drive, Urbana, IL 61801, USA
Tel: 217-265-5475
Fax: 217-333-5574
Email: bohnert@life.uiuc.edu
POLYA=Yes.

FEATURES

1. 659
/organism="Zea mays"
/mol_type="cDNA"
/db_xref="taxon:4577"
/clone_lib="zmrw48"
/notes="Samples were collected in Robert E. Sharp's lab (University of Missouri-Columbia) to construct three normalized cDNA libraries. Dark-grown maize seedlings to high primary roots 12-20 mm in length were transplanted to high (-0.03 MPa) or low water potential (-1.6 MPa) vermiculite, and harvested at 5 h and 48 h after transplanting. About 1,000 roots were used for each of the low water potential libraries (zmrw05 and zmrw48) while 500 roots were combined from each of the two time points at high water potential (zmrw00). Each root was divided into 4 segments (distances are from the junction of the root apex and root cap: segment 1, 0-3 mm plus the root cap; segment 2, 3-7 mm; segment 3, 7-12 mm; segment 4, 12-20 mm. [for details of conditions see (1) with nutrient modifications as in (2)]. The three normalized cDNA libraries were constructed in the lab of Hans Bohnert (University of Illinois-UC). Total RNA was extracted by the 'hot Phenol' method (Plant Molecular Biology manual, D5: 1-13, 2nd ed., 1997). This method worked in eliminating carbohydrate material present in the root tips. The integrity of the RNA was verified by denaturing agarose gels and spectrophotometry (ratio A260/280). Poly(A)+mRNA was isolated twice from total RNA using the Oligotex Direct mRNA kit (Qiagen). Poly(A)+mRNA was converted to double-stranded cDNA and lagged by using modified Oligo(dT) primers. One of 4 sequence tags corresponding to a different segment of the root was added to the 3'-end of the modified Oligo(dT) primers, including a NotI site and used to reverse transcribe the segment-specific mRNAs into cDNAs. Each library contains all four tags. A suffix (s1, s2, s3, or s4) has been added to each sequence identifier to designate which region of the root (Root segment 1, 2, 3, or 4) the sequence was found in based on the identification of the tag. A suffix of s0 indicates that the sequence tag, and hence the source segment, could not be identified. The double stranded cDNAs were size-selected (>450 bp). Size selected cDNAs were adaptorized with EcoRI adaptors at both ends, and then digested with NotI. The cDNA was directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene) and electroporated into E.coli DH10B. The total number of white colony forming units (cfu) in the primary libraries before amplification was as follows: zmrw05: 3.37 x 10⁶; zmrw48: 4.87 x 10⁶; zmrw00: 3 x 10⁶. The background of empty clones was less than 1%. Inserts ranged from -0.5kb to >2.5 kb, as determined by PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 300C. Non-hybridized single-stranded DNA circles were separated from hybridized DNA-rendered partially double-stranded and

Db 686 GGAGGAGTCCAAATTTCTCTCCACCAAGTAGCGCTCCAGCTCCAGCTTACATCATCCACCGCCGCA 745

Qy 660 TACCTTCGGTCTCCAGATCATCGAGG 688

Db 746 TACCTTCGGTCTCCAGATCATCGAGG 774

RESULT 5
 BG842003/c
 LOCUS BG842003 665 bp mRNA linear EST 29-MAY-2001
 DEFINITION MEST35-A02.T3 ISUM3-TL Zea mays cDNA clone MEST35-A02.3', mRNA sequence.
 ACCESSION BG842003
 VERSION BG842003.1 GI:14208332
 KEYWORDS EST.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (Bases 1 to 665)
 Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
 Expressed Sequence Tags from B73 Maize Seedlings and Silks
 Unpublished (2001)
 Contact: Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
 Tel: 515-294-0975
 Fax: 515-294-2299
 Email: schnable@iastate.edu
 PCR Primers
 FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)
 BACKWARD: T3 (ATT AAC CCT CAC TAA AG)
 Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
 Location/Qualifiers
 1..665
 /organism="Zea mays"
 /mol_type="mRNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST35-A02"
 /tissue_type="Seedling and silk"
 /lab_host="DH10B"
 /clone_lib="ISUM3-TL"
 /note="Vector: pT73PAC; Site 1: EcoRI; Site 2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5' AACTGCAAGATTCGGCGCCGAGAAATTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol-I catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector."

ORIGIN
 Query Match 49.2%; Score 657.6; DB 12; Length 665;
 Best Local Similarity 99.4%; Pred. No. 4.2e-106;
 Matches 660; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 673 TCCAGATCATCGAGCCGAGCGCTTGAGAACCCCAAAATTAAGTCTCTGGGACTCG 732
 Db 665 TCCAGATCATCGAGCCGAGCGCTTGAGAACCCCAAAATTAAGTCTCTGGGACTCG 606
 Qy 733 GAAGTTGTGAGGCTATGGCGCGCAACGGCGCCATTGGCTGGCGTAAGTTAAG 792
 Db 605 GAAGTTGTGAGGCTATGGCGCGCAACGGCGCCATTGGCTGGCGTAAGTTAAG 546
 Qy 793 AACCTACTGAATGGTGAAGTCTCGGATCTTCAGGTCTGGGCTCTCTTCGCCATCGGG 852
 Db 545 AACCTACTGAATGGTGAAGTCTCGGATCTTCAGGTCTGGGCTCTCTTCGCCATCGGG 486

Qy 853 CATGAGCCGCGGACCAAAATTCCTGGCGGACAGCTTGAATTCAGATTCAGATGTTATGTG 912
 Db 485 CATGAGCCGCGGACCAAAATTCCTGGCGGACAGCTTGAATTCAGATTCAGATGTTATGTG 426
 Qy 913 GAAACCAAGCCAGCTTCCACTCAGACAGTGTAAAGSGTGTATTCGCTGCGGACGTG 972
 Db 425 GAAACCAAGCCAGCTTCCACTCAGACAGTGTAAAGSGTGTATTCGCTGCGGACGTG 366
 Qy 973 CAGGACAAGAAAGTACCGTTCAGGGCCATTACTGCGCGCTGGATCAGGGTGCATGGCTGCAATTG 1032
 Db 365 CAGGACAAGAAAGTACCGTTCAGGGCCATTACTGCGCGCTGGATCAGGGTGCATGGCTGCAATTG 306
 Qy 1033 GAGCTGAGCAGCTACCTGCGAGGAGATCGGTGCGACAGGAGGGAAGTCTGATTCAGCTATAT 1092
 Db 305 GAGCTGAGCAGCTACCTGCGAGGAGATCGGTGCGACAGGAGGGAAGTCTGATTCAGCTATAT 246
 Qy 1093 TTAGTGTACCAACCAAGCAATCCATCGAATAGTCAGTTGTTCGGTGTGAAAGCGGCTCTC 1152
 Db 245 TTAGTGTACCAACCAAGCAATCCATCGAATAGTCAGTTGTTCGGTGTGAAAGCGGCTCTC 186
 Qy 1153 TGATGCGGTTTATGCCATCGGTTGTCATGAGCTCAGATTCAGATTCAGATTCAGATTCAT 1212
 Db 185 TGATGCGGTTTATGCCATCGGTTGTCATGAGCTCAGATTCAGATTCAGATTCAGATTCAT 126
 Qy 1213 GCTGCTTAGTAGCATGCTATTCTTATCGTTAGGATCCAGAAAGTATGTCGAACCTCGAAC 1272
 Db 125 GCTGCTTAGTAGCATGCTATTCTTATCGTTAGGATCCAGAAAGTATGTCGAACCTCGAAC 66
 Qy 1273 TATTTACTGGATACCTATTTCGTGATTACTGCTTGAAGTTTCTTCTTAGATATCAAAAAA 1332
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RESULT 6
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 LOCUS 946128A07.y1 946 - tassell primordium prepared by Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.
 ACCESSION BU036557
 VERSION BU036557.1 GI:22472077
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 SOURCE Zea mays
 ORGANISM Zea mays
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 1 (Bases 1 to 643)
 Walbot, V.
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 Unpublished (1999)
 Contact: Walbot V
 Department of Biological Sciences
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 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 946128 row: A column: 07.
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 /dev_stage="just after the transition from vegetative to inflorescence development"

FEATURES
 source

resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

ORIGIN

Query Match 51.2%; Score 684; DB 12; Length 705;
Best Local Similarity 100.0%; Pred. No. 9.3e-111; Indels 0; Gaps 0;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 670 GCTTCGAAGTATCATGCGGCGAGGCGCTTGAGAACCCCAAAATTAGCTCTCTGGAC 729
DB 645 GCTTCGAAGTATCATGCGGCGAGGCGCTTGAGAACCCCAAAATTAGCTCTCTGGAC 586
QY 730 TCGGAGTGTCTGAGGCGCTATGCGGCGCAAAAGCGGCGCCATTTGGCTGCGTAAAGGTT 789
DB 585 TCGGAGTGTCTGAGGCGCTATGCGGCGCAAAAGCGGCGCCATTTGGCTGCGTAAAGGTT 536
QY 790 AAGAACTACTGAATGTGAGGCTTCGGATCTTCAGGTGCTGGCTCTCTTCGCGCATC 849
DB 525 AAGAACTACTGAATGTGAGGCTTCGGATCTTCAGGTGCTGGCTCTCTTCGCGCATC 466
QY 850 GGCATGAGCGCGGCAAAATCTCTGGGCGGACAGCTTGAATTCGATTCAGATGCTAT 909
DB 465 GGCATGAGCGCGGCAAAATCTCTGGGCGGACAGCTTGAATTCGATTCAGATGCTAT 406
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DB 405 GTGGAAACCAAGCAGGTTCCACTACACCAAGTGTAAAGGGTGTATTGTGCTGCGGAC 346
QY 970 GTCGAGGACAGAGTACCTGAGGCGGATTCAGGCTGAGTACAGGCTGCAAGGCTGCA 1029
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DB 165 CTCTGATGCGGTTTATGCGGCTGCTGATGAGCTCAGGATGAGATACCTGATGATT 106
QY 1210 TATGCTGCTTAGTACGATGCTATCTTATGTTAGGATCCAGAGTATGCTGATCTCTG 1269
DB 105 TATGCTGCTTAGTACGATGCTATCTTATGTTAGGATCCAGAGTATGCTGATCTCTG 45
QY 1270 AACTATTACTGGATACCTATTTCG 1293
DB 45 AACTATTACTGGATACCTATTTCG 22

RESULT 4
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DEFINITION
CC658769 774 bp DNA linear GSS 19-JUN-2003
OCWEP74TH_ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0560N04,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CC658769.1 GI:32062228
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 774)
Whitelaw C.A., Quackenbush J., Van Aken S., Utterback T.,
Resnick A., Fraser C.M., Budiman M.A., Bedell J.A., Rohlfing T.,
Citek R.W., Nunberg R.A., Robbins D. and Lakey N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWEP74TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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DB 86 GAACGTGTAATTTTCAGATTTCAGAGGCGCGCAAGAACCTCTTTGACCAACGCGCGCGCGCG 145
QY 61 GCGAAGCAGCAAGCAAACTGAGTAAAGCAGCTATGAGGAGGATCCGCGCGCGCTCCGCTCCGC 120
DB 146 GCGAAGCAGCAAGCAAACTGAGTAAAGCAGCTATGAGGAGGATCCGCGCGCGCTCCGCTCCGC 205
QY 121 AGCGCATCTGATCATATGAGGAGCGGTCGCTGGCAGACGCGAGGATCTACCGCGGC 180
DB 206 AGCGCATCTGATCATATGAGGAGCGGTCGCTGGCAGACGCGAGGATCTACCGCGGC 265
QY 181 CGCGCGGAGCTCAAGCGCTGTGCTCTTCGAGGAGGCTGGATGGCCAAAGACATCCGCGCGGC 240
DB 265 CGCGCGGAGCTCAAGCGCTGTGCTCTTCGAGGAGGCTGGATGGCCAAAGACATCCGCGCGGC 325
QY 241 GGGCAGCTCACCACCAACCAAGCTCGAGAACTTCGCGGCTTCCCAAGCGGATCATG 300
DB 326 GGGCAGCTCACCACCAACCAAGCTCGAGAACTTCGCGGCTTCCCAAGCGGATCATG 385
QY 301 GGGCGGAGCTCATGAGCAACTCGCGCGAGTCCCTGCGCTTTGGCAACCAATCTCTC 360
DB 386 GGGCGGAGCTCATGAGCAACTCGCGCGAGTCCCTGCGCTTTGGCAACCAATCTCTC 445
QY 361 TCCGAGACCGCTCACCAGCGCTCGACTTTTCGCGCTTCCCAATCCGAGTTAGTGCAGATCC 420
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QY 421 ACAACGCTCTCGCGATCGGTTATCGTTGCCAGGAGCGGCTCGCGCGCGCTCCAC 480
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QY 541 GCGCGCGGCTCTCGGTTAAAGGAGGATCGCGGCTATGAGGCGGCGG- ACTCCGCTAT 599
DB 626 GCGCGCGGCTCTCGGTTAAAGGAGGATCGCGGCTATGAGGCGGCGGGAATCCGCTAT 685
QY 600 GGAGGAGTCCCAATTTCTCTCACCAGTACGCTTCCCAAGTCTACATCATCCACCGCGCAA 659

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES

source

Location/Qualifiers
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/db_xref="taxon:4577"
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/notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

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Query Match 98.5%; Score 1316; DB 11; Length 1380;
Best Local Similarity 99.5%; Pred. No. 2.4e-222;
Matches 1331; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

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QY 121 ACGCGCATCTGCATCATCGGAGCGCTCCGCTGCGCACACCGGACCCATCAAGCGCGCC 180
DB 153 ACGCGCATCTGCATCATCGGAGCGCTCCGCTGCGCACACCGGACCCATCAAGCGCGCC 212
QY 181 CGCGCGAGCTCAAGCTGCTCTTCGAGGCTGATGCGCAACGACATCGCGCGGC 240
DB 213 CGCGCGAGCTCAAGCTGCTCTTCGAGGCTGATGCGCAACGACATCGCGCGGC 272
QY 241 GCGCAGCTCACACCAACCGAGCTCGAGAACTTCCCGGGCTTCCCAACCGCATCATG 300
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DB 333 GCGCGGAGCTCATGAGCAACTGCGCGCGAGTCCCTCGCTTGGCACCAACATCCTC 392
QY 361 TCGAGACCGCTCACCGCGCTCGACTTTTCGCTGCGCCATTCGAGTTAGTGACAGCTCC 420
DB 393 TCGAGACCGCTCACCGCGCTCGACTTTTCGCTGCGCCATTCGAGTTAGTGACAGCTCC 452
QY 421 ACAACCGTCTCGCGATCGGTTATCGTTGCGACCGGAGCGCTCGCGCGCGCTCCAC 480
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DB 633 GAGGAGTCAATTTCTTCACCAAGTACGCTCCACGCTCATCATCATCCACCGCGCAAT 692
QY 661 ACCTTCGCTGCTTCCAAAGTATCATGAGCGCGCGCTTGGAGAACCCCAAAATTAAGGTC 720
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QY 1021 ATGGCTGCATTCGAGCGCTGAGCATTACTGCGAGGAGATCGGTGCGACAGAGGGAAAGTCT 1080
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QY 1261 T--GAACTCTGAACTATTATTACTGAGTACCTATTCGTGATTACTGCTTGAAGTTTTCCT 1318
DB 1293 TTGAACTCTGAACTATTATTACTGAGTACCTATTCGTGATTACTGCTTGAAGTTTTCCT 1352
QY 1319 TAGATATCAAAAAA 1336
DB 1353 TAGATATCAAAAAA 1370

RESULT 2
CG300268
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DEFINITION
OG2AB91TV ZM.0.7.1.5_KB Zea mays genomic clone ZM8MA0742013,
genomic survey sequence.
ACCESSION
CG300268
VERSION
CG300268.1 GI:34214482
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 871)
Whitelaw C.A., Quackenbush J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG2AE91TH
CONTACT: Cathy Whitelaw
TIGR Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: 7F
Class: sheared ends.
FEATURES
Location/Qualifiers
1. .871
source

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146	Qy	715	GCAATACCTTCCTGCTTCCAGATCATCAGCCAGGCGCTTGAGAACCCCAAAATTA
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161	Db	1075	AGAGTGAAT

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PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
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PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 32.5%; Score 434.6; DB 3; Length 1313;
Best Local Similarity 67.2%; Pred. No. 3.3e-89;
Matches 651; Conservative 0; Mismatches 304; Indels 14; Gaps 2;

second protein through a linker. The variant TRR protein has 1-3 amino acid substitutions as compared to the wild-type Arabidopsis TR protein. The amino acid substitutions are selected from positions A4, A5 and A6, preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5V, RA5Y, RA6S, RA6Q, RA6Y, and RA6N. The method is useful for reducing the toxicity of toxic proteins, reducing allergenicity of food and increasing the digestibility of food. The invention provides an efficient and low cost method as compared to prior art. The present sequence encodes a mutant A. thaliana TRR as an S-tagged/His-tagged fusion protein.

Query Match 32.6%; Score 435.8; DB 9; Length 6357;
Best Local Similarity 65.9%; Pred. No. 2.6e-89;
Matches 654; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

Qy	108	CGTCGCTCCGCA	CGGGCATCTGCATCAT	CGGAGGGGCTCCCGT	TGCGCACACGGCAGC	167
D _b	5345	CGAACTCACAA	CAAGGCTCTGTATCGT	TAGGAATGGCCAGCG	CGGCACACACGGCGGC	5404

168 CATCTACGGGGCCGGCGGAGGTCAGCCCTGTGCTCTTCGAGGGCTGGATGGCCACGA 227

5465 5464

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[illegible]

XXXXXXXXXXXXXXXXXXXXXXXXXXXX

[illegible]

5585 TACTACGATATTTACAGAGACGGTGACGAAAGTCGATTTCTCTTCGAAACCGTTTAAAGCT 5644

408 TAGTGCAGACTCCACAAACCGTCTCGCCGATGCGGTATCGTTGCCACGGGAGCGTCGC 467

Db
5645 ATTCACAGATTCACAGGCCATTCTCGTGACGCTGTGATTCCTGCTACTGGAGCTGTCG 5704

QY 468 GCGGGCTTCCACTTCCCGGTCCGATGCA-----TACTGGAACCGCGGCAT 515

D_b 5705 TAAGCGGCTTAGCTTCGTGGATCTGGTGAAGGTTCTGGAGGTTTCTGGAAACCGTGGAAT 5764

Qy 516 CTCGGCCTGTGCCGCTCTGTGACGGTGCCTGCCCGCCCCCATCTTCCGTAACAAGCCCATCGCCGT 575

D_b 5765 CTCGCAATGCGCTGTTTGGACGGAGCTGCTCCGATATTCCGTAAACCACTCTTGCGGT 5824

576 CATAGGCGCGGCGACTCCGCTATGGAGGAGTCCAATTCTCTACCAAGTAGCGCTCCCA 635

db 5825 GATCGGTGGAGCGCATTCAGCAATGGAAGAAGCAACCTTCTTACAAAATATGGATCCAA 5884

635 CGTCTCATTCTCTCCCGCGCAATACCTTCGCTGCTTCCAGATCATGCAGGCAGGCG 695

594A

755

[illegible][illegible][illegible]

816 GGATCTCAGGTCCTGGCCCTCTCTCCATCCGGCATGAGCCCTGGCAATTCCT 873

D5 6065 TGATTTAAAGTTTCTGGATTTGTTCTTGGCTATTTGGTCATGAGCCAGCTACCAAGTTT 6124

876 GGGCGGACAGCTTGAACTCGATTCAGATGGTATGTGGAAACCAAGCCAGGTTCACATCA 935

D_b 6125 GGATGGTGGTGTGAGTTAGATTTCGGATGGTTATGTTGTACGAAGCCCTGGTACTACACA 6184

936 CACCAGTGTAAGGGTGATTTGCTGCTGGCGACGTGCAGGACAAGAGTACCGTCAGGC 995

CC	minimizing oxidative stress and ischemic-reperfusion induced in acute
CC	lung injury. This polynucleotide sequence represents a thioredoxin
CC	reductase variant DNA sequence of the invention
XX	
SQ	Sequence 6357 BP; 1521 A; 1640 C; 1652 G; 1544 T; 0 U; 0 Other;
	Query Match 32.6%; Score 435.8; DB 7; Length 6357;
	Best Local Similarity 65.9%; Pred. No. 2.6e-89;
	Matches 654; Conservative 0; Mismatches 327; Indels 12; Gaps 1;
QY	108 CGCTCCGCTCGGACGGGATCTGCTCATCGGAGGCTCCGCTCGGCACAGCGCAGC 167
DB	5345 CGAACTCAACAACAAGGCTCTGTATCGTAGGAAGTGGCCAGCGCACACAGCGGCGC 5404
QY	168 CATCTACGGCGCCGCGGAGCTCAAGCTCTCTCTCGAGGCTGGATGGCCAAACGA 227
DB	5405 GATTTAGCGAGTAGGCTGAACCTTAACCTCTCTCTCGAGGATGGATGGCTAACGA 5464
QY	228 CATCGCGCGCGCGGAGCTCACACACACCGAGCTGAGAACTTCGGGCTTCCC 287
DB	5465 CATCGCTCCGCGTGTCAACTAAACACACCGAGCTGAGAAATTTCCCGGATTTCC 5524
QY	288 CAACGGCATCATGGCGCGGACCTCATGGCAACCTCGCGCGGAGTCCCTGCGCTTTGG 347
DB	5525 AGAAGGTAATTCGGAGTAGCTCACTGACAAATTCGTAACAACTCGGAGGATTCGG 5584
QY	348 CACCAACATCTCTCCGAGACCGTCAACCGCGTGCATTTTGGCGCTGCCATTCGAGT 407
DB	5585 TACTACGATATTTACAGAGCGGTGACGAAAGTCCGATTTCTCTCGAAACCGTTTAAGCT 5644
QY	408 TAGTGCAGATCCACAAACGCTCTCGCGGATGCGGATGCGGATGCGGAGCGCTCGC 467
DB	5645 ATTCACAGATTCGAAGGCATCTCGCTGACGCTGTGATTCGCTACTGAGGCTGTGGC 5704
QY	468 GCGCGGCTCCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGGCAT 515
DB	5705 TAAGCGCTTAGCTTCGTTGGATCTGGTGAAGGTTCTGGAAGCTTCTGGAACCGTGAAT 5764
QY	516 CTCGCGCTGCGCTCTGTGACGCTGCGCGCCCATCTTCGTAACAGCCATTCGCGCT 575
DB	5765 CTCGCGATGCGCTGTTTGGCAGGAGCTGCTCCGATATTCGTAACAAACCTCTGCGGT 5824
QY	576 CATAGGCGCGCGCACTCCGCTATGAGAGGATCCAAATTTCTCAACGAATGCGCTCCCA 635
DB	5825 GATCGGTGAGGCGCATTCAGCAATGAAGAAAGCAAACTTTCTTACAAATATGATGCA 5884
QY	636 CGCTACATCATCCACCGCCCAATACCTTCGCTTCCAGATCATGAGGCGCAGGC 695
DB	5885 AGTGTATATATCCATCGCTACGATGCTTTTAAATGCGCTTAAGATTTGACAGCGCGC 5944
QY	696 GCTTGAGAACCCCAAAATTAAGGTCCTCTGGGACTCGGAAGTTGTGAGGCGCTATGGCG 755
DB	5945 TTGTCTATCTAAGATTGATGTGATTTGGAATCGTCTGTGGAAGCTTATGGGA 6004
QY	756 CGCAACCGCGGCCCATTTGGCTGGCGTAAAGTTAAGAACTTACTGAATGTGAGTCTC 815
DB	6005 TGGGAAAGAGATGTGCTTGGAGGATTTGAAAGTGAAGAAATGTGTTACCGGTGATGTT 6064
QY	816 GGATCTTCAGTGTCTGCGCTCTTCTTCGCAATCGGCTAGCGCGGACCAAAATTCCT 875
DB	6065 TGAATTAAGATTTCTGATTTGTTCTTCTTATTTGCTTATTTGGTATGAGCCAGTACCAATTT 6124
QY	876 GGGCGGACAGCTTGAACTCGATTCAGATGGTATATGTGGAACCAAGCAGGTTCCACTCA 935
DB	6125 GGATGGTGTGTGATGTAGATTGCGATGCGATGTTATGTTGTCCAGAGCGCTGTACTACACA 6184
QY	936 CACAGTGAAGGTTGATTTGCTGCGCGGCACTGAGGACGAGAAAGTACCGTCAAGC 995
DB	6185 GACTAGCGTCCCGGAGTTTTCGCTGCGGGTGATGTTCCAGTAAAGATATAGCGAGC 6244
QY	996 CATTACTGCGCTGATCAGGCTGATGCGCTGCAATTTGGACGCTGAGCACTACCTGCGAGA 1055
DB	6245 CATCACTGCTGACGGAACCTGGGTGCAATGCGAGCTTTGGATGCGAGGCAATTACTTACAAGA 6304

QY	1056 GATCGTGCACAGGAGGAAAGCTCTGATTTGACT 1088
DB	6305 GATTGATCTCAGCAAGGTAAAGATGATTTGACT 6337
RESULT 13	
ADD26531	
ID	ADD26531 standard; DNA; 6357 BP.
XX	
AC	ADD26531;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Thalacress thioredoxin reductase RYN-M/S-tag/His-tag mutant DNA.
XX	
KW	Thioredoxin reductase; TRR; cofactor specificity;
KW	computational mutagenesis; substrate specificity; PDA;
KW	protein design automation; toxic protein; food allergenicity;
KW	food digestibility; thalacress; ds; mutant; plant.
OS	Synthetic.
XX	Arabidopsis thaliana.
XX	
PN	US2003100743-A1.
XX	
PD	29-MAY-2003.
XX	
PF	06-MAY-2002; 2002US-00141531.
XX	
PR	04-MAY-2001; 2001US-0289029P.
PR	05-APR-2002; 2002US-0370609P.
PR	29-APR-2002; 2002US-0376682P.
XX	
PA	(DALM/) DALMIA B K.
PA	(BRIG/) BRIGGS S P.
PA	(VALG/) VAL G D.
PA	(DESJ/) DESJARLAIS J R.
PA	(HEIF/) HEIFETZ P.
PA	(LUGI/) LUGINBUHL P.
PA	(MUCH/) MUCHAL U.
XX	
PI	Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
PI	Luginbuhl P, Muchhal U;
XX	
DR	WPI; 2003-801212/75.
DR	P-PSDB; ADD26551.
XX	
PT	Altering the cofactor specificity of thioredoxin reductase, useful for
PT	reducing the toxicity of toxic proteins, reducing allergenicity of food
PT	and increasing the digestibility of foods, comprises computational
PT	mutagenesis.
XX	
PS	Disclosure; Fig 16; 125pp; English.
XX	
CC	The invention relates to altering the cofactor specificity of thioredoxin
CC	reductase (TRR) comprising computational mutagenesis. Also included are
CC	altering the substrate specificity of TRR or cofactor specificity of a
CC	target protein, a variant TRR protein that reduces a protein that reduces
CC	a thioredoxin protein (obtained from an organism selected from
CC	Bacterichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,
CC	Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused
CC	to a second protein (that is either a wild-type TRR protein, thioredoxin,
CC	or a variant TRR protein), producing a plant with a modified TRR protein,
CC	a transformed plant prepared by the method and a transformed seed of the
CC	transformed plant. The cofactor specificity of the variant TRR is altered
CC	such that the variant preferentially binds NADPH compared to NADH, or
CC	vica versa. The protein design cycle comprises protein design automation
CC	(PDA (RTM)). This design cycle comprises the sequence design algorithm,
CC	or a force field calculation. The variant TRR protein is fused to the
CC	second protein through a linker. The variant TRR protein has 1-3 amino
CC	acid substitutions as compared to the wild-type Arabidopsis TR protein.
CC	The amino acid substitutions are selected from positions A4, A5 and A6,

		Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;			
QY	108	CGCTCGCTCCGACCGCGATCTGCATCATCGGAGCGTCCGCTGCGCACACGCGCAGC	167		
DB	5345	CGAAACTCACAACACAAAGGCTCTGTATCGTAGAGTGGCCAGCGGCACACACGCGCGC	5404		
QY	168	CATCTACGGCGCGCGCGAGCTCAAGCTCTGCTCTTCGAGGGCTGATGGCCAAACGA	227		
DB	5405	GATTTACGAGTAGTGGCTGAATTAACCTCTCTCTCGAAGATGATGGCTTAACGA	5464		
QY	228	CATCGCGCGCGCGCGAGCTCACACACACACACGAGCTGAGAGATTCCTCCGGGCTTCC	287		
DB	5465	CATCGCTCCGCGTGTCAACTAACACACACACGAGCTGAGAGATTCCTCCGGGATTC	5524		
QY	288	CAACGCGATCATGCGCGCGAGCTCATGACACACTGCGCGCGCTGCTCGCTTTGG	347		
DB	5525	AGAGGTATTCGAGTAGAGTCACTGACAAATTCGTAACATCGAGCGATTCGG	5584		
QY	348	CAACCAATCTCTTCGAGACCGTCAACCGCTTCGCTGCTGCTCCGCTCCGCTTCCGAGT	407		
DB	5585	TACTAGATATTACAGACGCGTACGAAAGTCTGATTTCTTCGAAACCGTTAAAGT	5644		
QY	408	TAGTCAGACTCCACACCGTCTCGCGATCGGCTTATGTTGCGACGGAGCGTTCGC	467		
DB	5645	ATTCAGATTCGAAGGCAATTCGCTGACGCTGATTCGCTACTGAGAGCTGTGCG	5704		
QY	468	GCGCGCTCCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGGCT	515		
DB	5705	TAAGCGCTTACCTTGGTATCTGTCAGAGTTCTGGAGTTCTGGAACCGTGGAT	5764		
QY	516	CTCCGCTCTGCGCTGTGACGCTGCGCGCGCTTCCTGTAACAGCCCATCGCGT	575		
DB	5765	CTCCGCTCTGCGCTGTGACGCTGCGCGCGCTTCCTGTAACAGCCCATCGCGT	5824		
QY	576	CATAGCGCGCGCTCTCGCTATGAGGAGTCCAAATTCCTCACCAAGTACGGCTCCA	635		
DB	5825	GATCGTGGAGCGATTCAGCAATGGAAGCAAACTTCTTACAAATATGATCCAA	5884		
QY	636	CGTCTACATCATCCACCGCGCAATACCTTCGCTGCTTCAAGATCATGCGCGCGC	695		
DB	5885	AGTGATATAATCATCCGCGCGCTTTCTGCTGCTCAAGATATGACGCGCGCGC	5944		
QY	696	GCTTGAGAACCCAAATTAAGTCTCTCGGACTCGGAAGTTGTCGAGGCTATGGGG	755		
DB	5945	TTTGCTTAATCTTAAGATGATGATTTGGAATCTGCTGTGTGGAAGCTTATGGAGA	6004		
QY	756	CGCAACCGCGCGCTTGGCTGCGGTAAAGTTAAGAACTTCACTCAATGCTGCTC	815		
DB	6005	TGAGAAAGAGATGTGCTTGGAGATTGAAAGTGAAGATGTTGTTACCGGTGATGTTT	6064		
QY	816	GGATCTTCAAGTGTGCTGCTCTTCTGCGCATCGGCTGAGCGCGGACCAAAATCTCT	875		
DB	6065	TGATTTAAAGTTTCTGGATTTGCTTTGCTATTTGTTCAAGCCAGCTTACCAAGTTT	6124		
QY	876	GCGCGGACAGCTTGAATCGATGTTATGTAAGCAACCAAGCCAGGTTCCACTCA	935		
DB	6125	GGATGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	6184		
QY	936	CACAGTGTAAAGGTTGATTTGCTGCTGCGACGTCGAGGACAGAAATCCGTCAGGC	995		
DB	6185	GACTAGCTTCCGAGTTTTCCTGCGGCTGATGTTTCAAGGATAGAGTATAGGCAAGC	6244		
QY	996	CATTCTGCGCTGATCAGGCTGATGCTGATGAGCGCTGAGCACTACTCTGACGA	1055		
DB	6245	CATCACTGCTGCGAACTCGGCTGATGCGAGCTTTGGATGAGAGCATCTTACAGA	6304		
QY	1056	GATCGGTGCACAGGAGGAAAGTCTGATGACT	1088		
DB	6305	GATTGGATCTCAGCAAGGTAAGAGTGTGAGT	6337		

RESULT 12
AAL54493

AAL54493 standard; DNA; 6357 BP.
AAL54493;
10-APR-2003 (first entry)
Thioredoxin reductase variant DNA sequence #15.
Ophthalmological; virucide; vulnerary; vasotropic; antiallergic;
cofactor specificity; thioredoxin reductase; TR; non-allergenic food;
computational mutagenesis; scaffold protein; oil body; animal feed;
digestibility; gluten; protein disulfide isomerase; PDI; enzyme;
scleroprotein; galled; food; nitrosative stress response; eye disease;
cataract; oxidative stress; ischemic-reperfusion; acute lung injury; ds.
Unidentified.
WO200290300-A2.
14-NOV-2002.
06-MAY-2002; 2002WO-US014358.
04-MAY-2001; 2001US-0289029P.
05-APR-2002; 2002US-0370609P.
29-APR-2002; 2002US-00370609P.
(XENC-) XENCOR.
(SYNC) SYNGENTA PARTICIPATIONS AG.
Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;
Luginbuhl P, Muchhal U;
MPI; 2003-111951/10.
Altering cofactor specificity of target protein, e.g. thioredoxin
reductase, useful for reducing antigenicity of glutens in wheat, barley,
or treating disulfide linkages present in proteins, by computational
mutagenesis.
Disclosure; Fig 16; 212pp; English.
The invention relates to a novel method for altering the cofactor
specificity of a target protein (e.g. thioredoxin reductase (TR)) by
computational mutagenesis. This method involves inputting a set of
coordinates for a scaffold protein comprising amino acid positions,
applying at least one protein design cycle, and generating a set of
candidate variant proteins with altered cofactor specificity. The novel
method is useful for altering the cofactor specificity of TR scaffold
proteins chosen from *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium*
leprae, *Saccharomyces*, *Neurospora crassa*, *Arabidopsis*, and human. Another
method of the invention is useful for making oil bodies which are useful
in the preparation of non-allergenic foods, or in the preparation of
animal feeds to improve the digestibility of the feeds. The variant TR
protein is useful for reducing the antigenicity of glutens in wheat, rye
or barley, to reduce alternative substrates for thioredoxin reductases,
including a number of plant and mammalian proteins found to contain
thioredoxin domains e.g. protein disulfide isomerase (PDI). The variant
TR protein is useful as a redox partner in compositions used for treating
disulfide linkages present in proteins such as enzymes, e.g., proteases,
amylases, etc., and structural proteins such as scleroproteins.
Compositions comprising variant TR proteins and PDI are useful for
generating protein disulfide crosslinks yielding high molecular weight or
gelled compositions, and thus is useful in food processing. A further
method of the invention is useful for producing plants with altered storage
TR protein, e.g., corn and soybean provides grains with altered storage
protein quality as well as grains that perform qualitatively differently
from normal grain during industrial processing or animal digestion of
variant TR proteins in combination with thioredoxin, which can be used to
manipulate nitrosative stress, to upregulate nitrosative stress
responses, and thus is useful for treating eye diseases, such as
cataracts, where it inhibits or reverse formation of cataract in eye. The
variant TR protein in combination with thioredoxin is also useful for